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I, KIM MARSHALL, MANAGER EXAMINATION SUPPORT AND SALES,
hereby certify that the annexed is a true copy of the Provisional specification in
connection with Application No. PP 4963 for a patent by CSL LIMITED filed on
30 July 1998.

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day of January 1999

KIM MARSHALL
MANAGER EXAMINATION SUPPORT AND
SALES



AUSTRALIA

Patents Act 1990

CSL LIMITED

PROVISIONAL SPECIFICATION

Invention Title:

P. gingivalis polypeptides

The invention is described in the following statement:

specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III) oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes.

In order to develop an efficacious and safe vaccine to prevent *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens to generate neutralising antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of *P. gingivalis* this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown *in vitro* it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism *in vitro* or produced in low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

In a first aspect the present invention consists in an isolated *P. gingivalis* nucleotide sequence, the nucleotide sequence consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1 to 22, fragments thereof and sequences complementary thereto.

5 In a second aspect the present invention consists in an isolated *P. gingivalis* polypeptide, the polypeptide being at least partially encoded by a nucleotide consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1 to 22, fragments thereof and sequences complementary thereto.

10 In a third aspect the present invention consists in an isolated *P. gingivalis* polypeptide consisting of or including an amino acid sequence selected from the group consisting of SEQ ID NO: 23 to 66 or fragments thereof.

In a fourth aspect the present invention consists in an isolated
15 polynucleotide, the polynucleotide encoding a polypeptide consisting of or including an amino acid sequence selected from the group consisting of SEQ ID NO: 23 to 66 or fragments thereof.

In a fourth aspect the present invention consists in a nucleotide probe specific for *P. gingivalis*, the probe including a detectable label and a
20 nucleotide sequence of at least 15 nucleotides, the nucleotide sequence being derived from a sequence selected from the group consisting of SEQ ID NO: 1 to 22 and sequences complementary thereto.

In a fifth aspect the present invention consists in a composition for use in raising an immune response in an animal directed against *P. gingivalis*
25 the composition including an acceptable carrier and/or adjuvant and at least one polypeptide having a sequence selected from the group consisting of SEQ ID NO: 23 to 66 or fragments thereof.

As will be understood by those skilled in the art the nucleotides of the present invention may be useful in DNA vaccination to reduce the incidence
30 and/or severity of *P. gingivalis* infection.

plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of Epicurian Coli Electroporation-Competent Cells (Stratagene) were transformed with the library DNA and plated out on SOB agar antibiotic diffusion plates containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

10 DNA sequencing

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a 96 well gridded array and stored at -20°C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Applied Biosystems). Raw trace data files from the ABI 377 sequencer were manually trimmed using Staden Pregap (Laboratory of Molecular Biology, Medical Research Council, UK) running on a Sun Microsystems computer. Trimmed files were assembled into contigs using Staden Gap v4.1 and exported as FastA consensus files.

DNA sequence data was supplemented with sequence downloaded from the Internet site of the Institute for Genome Research (<http://www.tigr.org>).

homology is present. Alternatively, protein coding regions may be identified using the ORF identification program GeneMark (3) using a matrix trained on published *P.gingivalis* sequences. This matrix may be further refined by adding ORFs identified from the results of homology searching and ORFs
5 identified by GeneMark. Otherwise, the program PSORT (4,6) may be used for the detection of signal sequences at the start of a protein and the prediction of cell localisation. A UNIX version of TopPred (5) may also be used to identify potential membrane spanning domains.

10 It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this thirtieth day of July 1998

CSL LIMITED

Patent Attorneys for the Applicant:

F B RICE & CO

Table 1

SeqID#	Length of SeqID	Homology description	Length of homolog	% identity	Overlap (aa)	E value
1,23,45	337aa	NplD lipoprotein, <i>Haemophilus influenzae</i>	379aa	38	120	7.80E-09
2,24,46	151aa	Hemolysin (TlyC), <i>Serpulina hyodysenteriae</i>	141aa	13	123	1.70E-07
3,25,47	391aa	Major outer membrane protein, <i>Pseudomonas aeruginosa</i>	350aa	26	382	3.30E-07
4,26,48	385aa	Major outer membrane protein, <i>Pseudomonas fluorescens</i>	317aa	29	233	2.20E-06
5,27,49	190aa	Potential membrane protein, <i>Rhodobacter capsulatus</i>	193aa	46	190	6.80E-32
6,28,50	833aa	Colicin I receptor, <i>Escherichia coli</i>	663aa	25	590	2.30E-10
7,29,51	891aa	Protective surface antigen, <i>Helicobacter pylori</i>	916aa	20	825	1.90E-10
8,30,52	170aa	Cationic outer membrane protein (ompH), <i>Yersinia enterocolitica</i>	164aa	27	168	4.40E-07
9,31,53	163aa	Cationic outer membrane protein (ompH), <i>Yersinia enterocolitica</i>	164aa	23	160	5.70E-05
10,32,54	827aa	Outer membrane protein (susC), <i>Bacteroides thetaiotaomicron</i>	1038aa	24	347	1.40E-06
11,33,55	390aa	Heme receptor (huta), <i>Vibrio cholerae</i>	693aa	24	368	6.80E-05
12,34,56	462aa	Outer membrane protein (tolC), <i>Escherichia coli</i>	481aa	20	425	1.60E-09
13,35,57	526aa	Neuraminidase, <i>Micromonospora viridifaciens</i>	647aa	32	375	2.10E-22
14,36,58	245aa	Outer membrane protein (omp28), <i>Brucella melitensis</i>	250aa	24	178	0.0015
15,37,59	276aa	Macrophage infectivity potentiator (mip), <i>Legionella israelensis</i>	242aa	35	219	8.80E-18
16,38,60	775aa	Outer membrane protein (omp85), <i>Neisseria meningitidis</i>	792aa	21	699	0.0036

Table 2 Results of protein analysis using Psort (6). Abbreviations used in the table are: OM = outer membrane, IM = inner membrane, PS = periplasmic space. * indicates an uncleavable signal sequence present.

Sed ID#	Signal present (Y/N)	Cleavage site	Cell location and probability		
			OM	IM	PS
67	Y	21	0.24	0	0.4
68	N	-	-	-	-
69	Y	20	0.62	0	0.13
70	Y	26	0.81	0	0.31
71	Y	13	0	0.5	0
72	Y	22	0.94	0	0.37
73	Y	40*	0	0.31	0
74	Y	20*	0	0.35	0
75	Y	18	0.21	0	0.93
76	Y	36	0.93	0	0.25
77	N	-	-	-	-
78	Y	27	0.25	0	0.54
79	N	-	-	-	-
80	Y	22*	0	0.38	0
81	Y	24	0.15	0	0.89
82	Y	23	0.79	0.7	0
83	Y	27	0.73	0	0.22
84	Y	24	0.94	0	0.38
85	Y	24	0	0.1	0
86	Y	18	0	0.12	0
87	Y	21	0.94	0	0.34
88	Y	25	0.2	0	0.61

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

5 (A) NAME/KEY: misc feature

(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

10	CCGAGCAAAA	CGATAATTAA	GACAATGGCA	AAAATCAATT	TCTATGCTGA	AGGCGTCAGC	60
	CTTCCTCGGA	TCAGAAGACG	GATCGTCGGT	AAGTGGATAG	CCGAAGTATG	CAGCCGATAT	120
	GGGAAAGCGG	TGGGAGAAAT	CTCCTATCTT	TTCTGTGATG	ACGAATATAT	CCTGAAAGCC	180
	AATCAGGAAT	TTCTCGATCA	TGACTACTAC	ACCGACATCA	TCACCTTCGA	TTCCTGCGAA	240
	GCGGATACGG	TGAATGGCGA	CCTGCTTATC	AGTCTCGATA	CCGTACGCTC	GAATGCCCGT	300
15	GCTCTTGATC	TTCGATACGA	AGACGAACTG	CATCGTGTCA	TTATCCACGG	CATACTGCAT	360
	CTTTGCGGAT	TGAAAGACAA	GAGCAAAAAG	GATGAAGCCC	AAATGCGTGC	AGCCGAAGAG	420
	AAAGCCCTTG	TCATGCTGCG	AGAAACCATC	GGATCGGAGC	TTTCCCTATT	GCATACA	477

20 (2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1185 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1185

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

	AAAAGTAAAA	CTATGAAGGT	AAAGTACTTA	ATGCTCACAT	TGGTTGGAGC	AATTGCACTG	60
	AACGCAAGTG	CACAGGAGAA	TACTGTACCG	GCAACGGGTC	AGTTACCCGC	TAAGAATGTT	120
45	GCTTTTGCTC	GCAATAAAGC	AGGCAGCAAT	TGGTTTGTA	CACTGCAAGG	CGGTGTTGCA	180
	GCGCAGTTCC	TCAATGACAA	CAACAACAAA	GACCTCATGG	ACCGCTTAGG	AGCCATAGGT	240
	TCTCTTTCTG	TCGGAAAGTA	TCACAGCCCT	TTCTTTGCAA	CTCGTTTGCA	AATTAACGGA	300
	GGTCAAGCCC	ACACTTTCCT	CGGAAAAAAT	GGCGAACAAG	AAATCAACAC	CAATTTTGGT	360
	GCAGCTCACT	TCGACTTTAT	GTTTGATGTG	GTAACTACT	TTGCACCATA	TCGCGAAAAT	420
50	CGTTTCTTCC	ATTTAATTCC	ATGGGTAGGT	GTTGGCTACC	AACACAAATT	CATCGGTAGC	480
	GAATGGAGCA	AAGACAATGT	GGAATCACTG	ACGGCGAATG	TAGGAGTTAT	GATGGCTTTC	540
	AGATTAGGAA	AGCGAGTAGA	CTTTGTGATC	GAAGCACAAG	CAGCTCACTC	CAATCTCAAT	600
	CTAAGTCGCG	CATACAATGC	CAAGAAAAC	CCCGTATTCG	AAGATCCCGC	AGGACGTTAT	660
	TACAATGGAT	TCCAGGGGAT	GGCTACAGCA	GGTCTTAATT	TCCGCCTGGG	AGCCGTAGGC	720
55	TTCAATGCCA	TTGANCCAAT	GGACTACGCA	CTTATCAATG	ATCTGAATGG	TCAGATTAAAC	780
	CGTTTGCGCA	GCGAGGTCGA	AGAACTCTCA	AAACGTCCTG	TATCATGCCC	CGAATGTCCT	840
	GAAGTAACTC	CTGTTACTAA	GACAGAAAAT	ATACTGACGG	AAAAAGCTGT	ACTGTTCCGT	900
	TTCGACAGCC	ACGTTGTGGA	CAAAGATCAA	TTGATCAACC	TGTATGACGT	AGCTCAGTTT	960
	GTAAAAGAAA	CTAACGAGCC	GATTACCGTT	GTTGGTTATG	CTGATCCTAC	GGGTAATACT	1020
60	CAATACAACG	AGAAATTGTC	TGAGCGTCGG	GCTAAAGCCG	TTGTTGATGT	TCTGACAGGT	1080

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
5      (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...585
10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

15  GTAATTGGCA TCATTATGGA ATTTTTCATG TTATTCATAG CGGCGGTTTT CGTTAATAAC      60
    GTCGTGCTGT CGCAGTTCCT CGGTATATGC CCATTCTTAG GCGTATCGAA GAAGGTAGAC      120
    ACCTCAATCG GTATGGGTGC AGCCGTGACA TTCGTATTGG CACTGGCTAC CTTGGTTACC      180
    TTCTGATTC AGAAGTTCGT TTTGGATCGT TTCGGATTGG GCTTTATGCA GACCATTGCA      240
    TTTATTTTGG TCATTGCCGC CTTGGTGCAG ATGGTGGAGA TCATACTCAA GAAAGTATCT      300
    CCTCCCCTCT ATCAGGCACT GGGTGTATTC TTGCCCTTGA TTACGACGAA CTGCTGTGTG      360
    CTCGGTGTGG CTATTTTGGT TATCCAGAAG GATTATACCC TGCTCCAGAG CTTTCGTCTAT      420
20  GCAATATCCA CGGCTATCGG TTTACCTTG GCAATGGTTA CTTTCGCAGG TATTTCGAGAG      480
    CAACTCGATA TGACCAATCT CCCCAAAGCT ATGAAGGGAA TACCTTCGGC ACTCTTGGCT      540
    GCCGGTATAT TGGCTATGGC TTTTCATGGG TTCAGCGGTA TCGCC                      585

25  (2) INFORMATION FOR SEQ ID NO:6

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2628 base pairs
          (B) TYPE: nucleic acid
30      (C) STRANDEDNESS: double
          (D) TOPOLOGY: circular

      (ii) MOLECULE TYPE: DNA (genomic)

35      (iii) HYPOTHETICAL: NO

      (iv) ANTI-SENSE: NO

      (vi) ORIGINAL SOURCE:
40      (A) ORGANISM: Porphyromonas gingivalis

      (ix) FEATURE:
          (A) NAME/KEY: misc_feature
          (B) LOCATION 1...2628
45

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

50  TACCGATCTT ATCGTGGGAT AGGGAGTGGG ACACACTCTC CTAACCTCAA AAACCGACTA      60
    AAAAGGATCG GAATAAGGAT ACCGAACAGA CACTATATCC ATATCAAGCC AATCAAACCA      120
    AAAAATAAAA TGAAACAACCT AAACATTATC AGCTTCATCA TTGCTTTCCT ATTCTTAGGA      180
    ACGAGCGCAT CGGCTCAGCA ATCGGGCGGA TCCGTTACAG GTACCGTAGT GGACAAAAGC      240
    TCAAAAGAAC CTATCGCATA CGTACAAGTA TTCGTCAAAG GAACCACTCT CGGAACCTTC      300
    ACGGATGCAA ACGGAAACTA CTCGATCAAG GGAATCCCTT CGGGTAATCA AACTATCGTA      360
    GCCCCGACTCA TGGGTTACTC CACTTGCGAA GAAAAAGTAC ATATAGAAAA GGGTGGTTCC      420
55  CGCCACGTAG ACCTCTATCT GACCGAAGAG ATTCTCTCTC TCGATGGGGT AGTGGTATCT      480
    GCCAATAGAA ACGAGACTTT CCGCCGTCAA GCACCTCGT TGGTAACGGT ACTGTCGCCG      540
    GAACTTTTCC TCAAAACCAA CTCTACCAAC CTGAGTCAGG GACTTAAGTT CCAGCCCGGT      600
    CTGCGCGTGG AGGACAACCTG TCAGAACTGC GGTTCCAACC AAGTTCGTAT CAATGGACTC      660
    GAAGGAGCCT ATTCGCAAAT TCTTATCGAC AGCCATCCCA TCTTCAGTTC GCTTGCCGGT      720
60  GTCTATGGCT TGGAGCAGAT GCCTGCCAAT ATGATCGAAC GTGTAGAAGT AATTCGCGGT      780

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	GATGAAGTCC	TGATTCTCTGG	AGATGCCATG	TCTGCTGCCG	TGAATAGAAT	TATGCGTCAG	300
	GGCTACTTCT	CAAATGTGCG	AATCATCGCG	GATAAATATG	TCGGCAATAA	AGTCTATCTG	360
	AAAATCATTG	TCACTGAACG	TCCTCGCATC	AGTAAGGTTA	CTTTTAGCGG	GGTAAAGAAG	420
	TCTGAGAGAG	AAGATCTTGA	AATGAAAATC	GGTCTTCGCG	AGGGGATTCA	GATGACCAGA	480
5	AATAATGAAG	ACAAGGTCAG	GCAAATCGTA	CAGAAGTATT	TTAGTGAGAA	AGGTTATCGC	540
	GATGCCAGCA	TACGGATAAC	GCAGGAACCG	GATCTTTCCA	AAGATGGCTT	TGTCATATGTG	600
	CTTATCTCGA	TTGAGAAGAA	AAGCAAAACC	AAGGTGAATG	AAATTTATTT	TTCCGGCAAC	660
	AAGGCCCTTA	GCAATCATAA	GCTAAGAATG	GCGATGAAGA	ACACCAATGC	CAAATTCAGT	720
	CTTAGAAAGC	ATATTCGCTC	ATCTTTCTTG	AACTTTTTTA	GTACTCATAA	GTTTGTGGAA	780
10	GAGAGCTACC	GTGAAGATTT	GGTCCGATTG	ATAGAGAAGT	ATCAGGAATA	TGGATATCGT	840
	GATGCTGAAA	TACTGACCGA	CAGTGTCTGT	AAGGCTCCTG	ACGGCAAAAG	AGTGGATATT	900
	TATCTCAACA	TCGAAGAGGG	GCAGAAGTAT	TATATTAAGG	ATGTCAACTT	TGTGGGCAAT	960
	TCACAATATC	CATCGGAGTA	TTTGGAACGA	GTGCTCGGAA	TAAATCCGG	AGATGTGTAC	1020
	AATCAGAGAC	GATTGGCTAA	GCGTCTCAAT	GAAGATGAAG	ATGCTGTGGG	GAACCTGTAC	1080
15	TATAACAATG	GCTATATTTT	TGCGTGGGTC	GATCCCGTGG	AAACAAATGT	AGTGGGGGAT	1140
	TCTGTTTCGC	TTGATATTCG	TATAGCGGAG	GGGAAGCAGG	CCAATATCAA	TAAGGTGATC	1200
	ATCAAAGGAA	ATACTGTCTG	GTACGAAGAC	GTAGTACGCC	GAGAGCTTTA	CACAAAGCCC	1260
	GGCCAGCTCT	TTAGTCGCGA	GGATATCATT	AAGCTTATTC	GTCTCATCAA	TCAGCTTGGG	1320
	CATTTTCGATG	CCGAAAATC	TATTTCCCGT	CCGATTCCCA	ATCCCAGAAC	AGGAACAGTG	1380
20	GATATAGAGT	ATGATTTGGT	GCCGCGTAGC	AGTGACCAAT	TGGAGCTTTC	TGTCGGTTGG	1440
	AGTCAGTCCG	GACTTCTGTT	CCGAGGAGCC	ATTAAGTTCA	CGAACTTCTC	TGTCGGCAAC	1500
	TTGCTCCATC	CCTCGATGTA	TAAGAAAGGG	ATCATTCCGC	AAGGGGATGG	GCAAACACTA	1560
	TCAGTGAAGT	CTCAGACCAA	TGGAAAGTAC	TATCAGCAGT	ATAGTGTAC	ATTTATGGAT	1620
	CCATGGTTTTG	GGGGCAAGCG	GCCGGATATG	TTCAGCTTCA	GTGCATTCTA	TTCCAAGACT	1680
25	ACGGCGATTG	ACTCCAAGTT	CTACAATAGC	AATGCCGGCA	ACTACTATAA	TGCCCTACTAT	1740
	AATAGCTACT	ACAACAACCTA	TAATAGTTAT	TACAACGGTA	TGTCGAACTA	TACCGGCGAC	1800
	CTCTATACTC	AGGCCAGCGA	TCCGGATCGT	TGCTTTCAGA	TGTTAGGTAC	TTCGATCGGT	1860
	TACGGTAAGC	GTTTGACTTG	GCCGGACAAT	TGGTTCCAGA	TTTATACTTC	TCTGAACCTAC	1920
	ACCTACTATA	GACTGCGAAA	TTGGAGCTAC	AATACCTTCC	AAAATTTCCA	TCATAGGCTCG	1980
30	GCTAATGATC	TCAACTTGGA	GCTGCGTCTC	TCTCGTACTT	CCATCGATAA	TCCTATTTAT	2040
	ACCAGAAGCG	GATCGGATTT	CATGGTTTTCT	GTTGCTGCTA	CTCTTCCTTA	TTCTTTGTGG	2100
	GACAATCATG	ACTATGCCAG	CCAGAACCTC	AGCGTAAGCG	ATCGTTACAG	ATTTATCGAG	2160
	TATCACAAGT	GGAAGTTTAG	AGGACGAGTT	TTTACTCCAT	TGCTCAATCC	TGCTACGCAT	2220
	AAATATACAC	CGGTGCTCAT	GAGTCGAGTG	GAAGGAGCAG	TTCTTGGTTC	GTATAATTCC	2280
35	AATAAGAAAT	CTCCTTTTCG	TACTTTCTAT	ATGGGAGGTG	ATGGTATGTC	CAGCTATTAT	2340
	GGTGGCTACA	TGAATGAGAC	TATAGGTTTG	CGTGTTTATA	AGAACGGATC	TATTGCCGGT	2400
	AATAACTACG	ACTATGCATA	TGCTTATATG	CGGCTTACGA	TGGAACCTACG	TTTCCCGATT	2460
	CTGTTTGAAA	ACTCATTCAA	TGCGTGGCTC	TTAGCTTTTG	CCGAAGCAGG	CAATGCGTGG	2520
	CGCAGTATCG	ACAATTATAA	TCCCTTTAAC	CTGAAGCGAT	CGGCCGGTGT	AGGATTGCGT	2580
40	GTAACGTTAC	CGATGGTCGG	AATGCTCGGT	ATCGATTGGG	GATATGGCTT	TGACCGTCCG	2640
	GACAATTCTC	TACAGCGAGG	AGGAAGCAAT	GTCCACTTTG	TGCTCGGACA	GGAGTTC	2697

(2) INFORMATION FOR SEQ ID NO:8

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

60

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...531

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

	CAAATAAACA TGAATGGCGA TATGAAACGG TTTTGTGATTT TGATCGGCTT TGCACTGGCG	60
	G TAGCTTTTCT CCGGTTTTTC CCAAAAGTTC GCTTTGGTAG ATATGGAATA TATCCTCAGG	120
	AATATTCCTG ACTATGAGAT GATGAACGAA CAGCTGGAAC AGGTGTCCAA GAAATGGCAA	180
10	AATGAAATCG AAGCTCTCGA AAATGAAGCC CAATCTATGT ATAAGAAGTA TCAGAGCGAT	240
	CTCGTATTCT TGTCTGCTGC ACAGAAGAAA ACCCAAGAAG AGGCTATCGT AAAGAAAGAG	300
	CAGCAAGCAT CCGAGCTCAA GCGGAAGTAT TTCGGCCCGG AGGGGGAGCT GTATAAGAAA	360
	CGCTCCGATC TGATGAAGCC TATTCAGGAT GAGATTGGA ATGCTATCAA AGAGATTGCC	420
	AAGCGTAACA ACTATCAGAT GGTGCTTGAT AGAGGTACGT CCGGAATTAT CTTTGCCAGT	480
15	CCGTCTATTG ACATTAGCGA CCTTGTACTG AGCAAGATGG GCTTTAGCAA G	531

(2) INFORMATION FOR SEQ ID NO:9

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- 25 (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- 30 (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Porphyromonas gingivalis*

- 35 (ix) FEATURE:
- (A) NAME/KEY: misc feature
 - (B) LOCATION 1...510

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

	CGAATAAATA AACAAACACGA AATGAAGAAA TTTTCTCTCA TGCTTCTGAT GGCTCTTCCT	60
	TTGAGCCTCT TGGCACAAAA GGTGGCAGTG GTAAACACTG AGGAGATCAT TTCCAAAATG	120
	CCGGAACAAG TAGCTGCTAC CAAACAGCTC AACGAATTGG CCGAAAAGTA TCGCCTTGAT	180
	CTCAAGAGTA TGGACGATGA GTTTGCCAAA AAGACAGAAG AATTTGTAAA GGAAAAAGAC	240
45	TCTCTACTGG AGAACATCCG CAATCGTCGT CAGCAGGAAC TTCAGGATAT TCAAACCTCGT	300
	TATCAGCAGT CATAACAAAC GATGCAGGAG GATTTGCAA AGCGCCAACA ACAGCTTTTT	360
	GCTCCTATCC AACAAAAGGT GGCTGATGCC ATCAAGAAAG TGGGTGACGA AGAAAACGTG	420
	GCCTACATCA TGGAGGCCGG TATGATGCTT TACACCGGAG CTACTGCTAT TGACTTGACC	480
50	GCAAAGGTAA AAGCGAAACT CGGAATCAAG	510

(2) INFORMATION FOR SEQ ID NO:10

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- 60 (ii) MOLECULE TYPE: DNA (genomic)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1191 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

AGAAATCGGA	GAACATAAAC	AATGCCGATC	CCACCGGTTT	CATCAACTAC	AAAAGCGACT	60
ACTACACCTA	TGGTGCCCTA	CTCCAGGACA	AGATTTCCCT	TGGAGGACAA	AAATATCGTA	120
CTCGGTGTCG	ACAGCCGAAA	CATGACGATG	GAGTCAGAAA	GATTCGAGCA	GGCAGGAGTG	180
25 AATACAAAGC	CATACAACCC	CGGATATGCC	ACGAACAATA	TCGGTTTGTT	CGGACAGGCC	240
AATTTCTACC	TGCTGAACGA	TGCTCTATCG	ATATCTGCCG	GTGCACGTGC	CGACTTCATG	300
TTCTTTGACC	TGAAAGCGAA	CGAGTATCTC	AACAATGAAG	CCAAACAGGA	AACTCATAAC	360
GTAATCAATC	CGAATGTCGG	AATCAAATAT	GAGTTTGTGA	AAGGCCTTAC	AGCTCATGGT	420
ACATTCCGTA	GTGCATTGAG	TGCTCCCGAT	GCTTTCCAAA	AAGCAGGCCA	ATACGTAGGC	480
30 CCGTTCGGCA	CGACCATAGG	CAATCCTGAC	CTGAAACCCG	AAAAGTCCAT	GACCTGGGAC	540
TTCGGTATCG	GATACAGCAA	TGCACGCTGC	GGGATCCAAG	CCGACGTAAC	CTTAACCTAT	600
TTCCACACCG	ACCACAAAGA	TCTGATCTTG	TCCAGCCCTG	ACTATGCTAA	TAATATCACC	660
ACATACATCA	ATGCCGACAA	GGCTCGTATG	AGCGGTATCG	AGGCCCTTTT	GTCTTATGAC	720
TTCGGCAGCC	TCTTTGCCAA	CAAGTTCTCT	CTCCGCGCAT	TTGCGAATGC	CACGATCATG	780
35 CTCAATTCCG	AGATGAAGAA	AAGCCAGACC	GATGCCCCCT	GGAGCGAAAT	GTACTACGTT	840
CGCAAGCAGA	ACATCACCTT	CGGTATCGAA	TATCGTGCCA	AAGAAGGACT	TGAAGTGATG	900
CTCAACGGTC	GCTTCATGGG	ACGCAGGATC	GAGCAAAACT	GGTATGCTTA	CTACCCCGAA	960
GTTCCGCCCC	AACTCCAGCA	ACTGCTTGCA	GCAGAAGAGC	CTGAATTGGC	TGCTCAGGGA	1020
CTGCTCCGTC	ATCCGCAAGC	AATGGTGTTT	AATGCCTCTG	CTTACTACCA	CATGAACAAG	1080
40 TATCTCACCT	TCGGTGTGAA	CTTGAACAAC	ATCTTGATG	AGCTTTATAE	GGAGAAAGAC	1140
GGCTACCACA	TGCCCCGACG	TAACATCATG	GGTAAGGTTA	TGGTCAACTT	C	1191

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1452 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*

	ATTCGTATCG	GATTCTCTCT	TCCGAAAGAA	ACGGAGGAAA	AAGTCACCGC	CCTATATCTC	300
	CTTGTGAGTG	ATTCTTTAGC	GGTGCGCGAC	TTGCCGGACT	ACAAAGGGCG	AGTCTCTTAC	360
	GATAGCTTCC	CGATCTCAAA	GGAAGATCGT	ACCACAGCCC	TTTCTGCGGA	TTCCGGTAGCC	420
	GGACGCCGCT	TCTTTTATTT	GGCTGCGGAT	ATAGGGCCTG	TTGCTTCTTT	TTCCCGATCC	480
5	GATACGCTGA	CTGCCCCTGT	GGAAGAGGTG	GCTGTGCGATG	GCCGCCCTTT	GCCGTTGAAA	540
	GAGCTGTGCG	CTGCCTCCCG	TCGTCTGTAT	AGGGGGTATG	AGGCCCTCTT	TGTACCCGGT	600
	GATGGCGGAT	CGCGGAACTA	TCGTATCCCG	GCCATTTTGA	AAACGGCTAA	TGGAACACTC	660
	ATAGCGATGG	CCGACAGACG	AAAATATAAT	CAGACGGATC	TGCCGGAGGA	TATAGATATA	720
	GTCATGCCGC	GCAGTACGGA	CGGAGGGAAA	TCGTGGAGCG	ATCCCAGGAT	TATCGTACAG	780
10	GGAGAGGGGC	GCAATCATGG	CTTTGGCGAT	GTAGCCCTGG	TGCAAACCCA	AGCAGGAAAG	840
	CTCCTGATGA	TCTTTGTCGG	TGGAGTAGGC	CTGTGGCAGT	CTACCCCCGA	TCGTCCTCAG	900
	CGCACTTATA	TATCGGAAAG	TCGGGACGAA	GGACTGACTT	GGTCGCCTCC	TCGGGATATA	960
	ACCCATTTC	TCTTCGGCAA	GGATTGTGCC	GATCCGGGAC	GCAGTCGCTG	GTTGGCCTCC	1020
	TTTTGTGCTT	CGGGACAAGG	GCTTGTGCTG	CCATCCGGTC	GTATCACGTT	TGTGGCTGCC	1080
15	ATCCGCGAAT	CAGGGCAGGA	GTACGTCTCT	AACAACATAG	TCCTCTATAG	CGACGATGAG	1140
	GGCGATACAT	GGCAGCTTTC	CGACTGTGCA	TACCGCCGTG	GCGATGAGGC	AAAGCTTTCA	1200
	TTGATGCCCG	ATGGCAGGGT	ACTGATGAGC	ATACGCAATC	AGGGACGGCA	GGAGAGCCGA	1260
	CAGCGTTTCT	TCGCTCTCTC	CTCCGACGAT	GGCCTTACTT	GGGAGAGAGC	CAAGCAGTTC	1320
	GAGGGCATCC	ATGACCCCCG	CTGTAATGGA	GCTATGCTTC	AAGTGAAAAG	GAACGGAAGG	1380
20	GATCAAGTGC	TGCACTCCCT	GCCTCTCGGC	CCGGATGGGG	GTCCGCGATG	AGCTGTCTAT	1440
	CTCTTCGATC	ATGTCTCCGG	CCGCTGGTCC	GCTCCCGTTG	TTGTCAATTG	AGGATCGAGT	1500
	GCCTACTCGG	ATATGACTCT	GCTGGCGGAT	GGAACGATCG	GTTATTTTCG	CGAAGAGGGC	1560
	GATGAGATCT	CATTGGTTTT	CATTCCGGTTC	GTCCTTGACG	ATCTCTTCGA	TGTCCGGCAA	1620

25

(2) INFORMATION FOR SEQ ID NO:14

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

50	AAGTCTCCGA	GCGATTCCGG	TTTGCCGTCG	GTATGGAGCG	CGAATACAAT	ATCTGGACTC	60
	GTCGGTGGGA	AACGCATTAC	TTTGCTTATC	CTGTATTCTA	TGGCGATAAG	AAGTAGTAAT	120
	ATAGAATCAA	TACAGTGCTT	TGTGATGAAA	AAAGAAAAAC	TTTGGATTGC	GATCGTCGCC	180
	GGTTTGGCTT	TCGTATTGGG	CCTTTATGCT	CTTGCCCGCA	GTGTCGCTCA	GCTACGCCGC	240
	TCTCAGCCTT	CGGTGACTGT	GACCGGTATG	GCCGAGCGTA	ATTTCAAATC	CGATCTGATC	300
55	GTTTGGACTG	CTTCGTACCA	GCTCCAGATG	ATGGATCTCG	AATCGGCCTA	CAAGGCTTTG	360
	AAGGAAAAAC	AGATATTGGT	AGCAGACTAT	TTGAAAAACA	AGCAGCTGCC	CGATTCTGCT	420
	TATATCTTCT	CAAGCGTAGC	CATCTCTAAA	GAATACAAC	ACTATTACGA	TCCTCGGCAG	480
	GAACAAAACG	TCAGGACCTT	TGCCGGGTAT	CTGCTCAGCC	AGACAGTTAC	GGTGACCTCA	540
	CAGGACATCG	AACATGTGGA	GAAAATATCT	CGCGATATAA	CGGAGCTGAT	CAATCAGGGG	600
60	GTAGAGATTA	CCTCCGACCG	TCCGGCCTAT	TACTACACCA	AGCTCAATGA	TCTGAAGGTG	660

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- 5 (A) NAME/KEY: misc_feature
(B) LOCATION 1...2409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

```

10  TGTCGAAAGC AGAAGCTCTC AAACCCGAAG AGGAGCCGGT ATCCGTGCAG ACGGATATCA      60
    TTCCGACAAA GCGATAAGAA TCCGATGAAA GTATTACGGC AAGTATTCCT CCCCATCCTT      120
    TTTGTCCCTAC TGACAGGTGC CTGCTCCACC ACAAAGAATC TGCCGGAAGG CGAACAGCTG      180
    TATATCGGAA TGGGCAAGAC ACAGATACTC CGGCAGGACA AGAGCCACGC CGGCCAACAG      240
    GCTCTGACCG AAGTGGAGAG TACACTGAAA GTTACACCCA ATGGAGCTAT TTTCGGCAGT      300
15  GCAAGTGCCCT CCTTACCCAA GATACCATTG GGGCTATGGC TATACAACAG CTTTCGTGGG      360
    GATTCCACTG TCATTTTCGAA ATGGATATTG GACAAGTTTG CAGCCAAGCC GGTTTTTCATC      420
    AGTCAGGTCA AATCCGATAG CCGGGCTAAG GTGGCGACGA ACATCCTCCG CGAACACGGG      480
    TACTTCGATG CTAAAGTAAA AAGCAGTGTG ACCACTCTGA AAAAGGACTC GCTCAAAGCC      540
    AAAATCTCCT ATACGGTGGA TATGGCCTCT CCTTATCATT ACGACAGCAT CATTCCCTTA      600
20  CCGATCAGCA CTTTCCCCGA CAGCATTCTG GCTTACAGGC AGACTCCGTC TTTGATCAGG      660
    AAAGGAGACC AGTTCAATTT GGCAAAGCTG CACGAAGAGC GTCAGACCAT CAGTGGCCTG      720
    CTGAGAGACA ATGGTTACTA CTACTTCCGC CCACAGGATA TTATCTACGA AGCCGATACC      780
    CTCCTCGTAA GAGGTGCCGT ATGCCTGCGA GCCAAGCTCT CGGAAGATAC TCCACCCCAA      840
    GCCATGCGCC CGTGGAGGAT AGGGAAACGG ACAGCAGTCC TGCTCGGAAT GAACGGAGAA      900
25  AGCCCAGCAG ACTCGCTCGA AGTGGAGGAT ATGAAAGTCC TTTACTATCG TAAAATGCCG      960
    GTTCGCCCCA AGATTTTGGC CAAACGCTTT CGTTTCTTCT CCGGCAATCT GTATCGGCAG      1020
    AAAGACGATG AGACGACACG CAAATCCTTG GCTCGTTTGG GAGCCTTCTC CGTTATCGAT      1080
    CTCAATTTT TGCAACGCGA TTCCATTTCG GGCTTTTGG ATGTGCGACT GCTAACCACC      1140
    CTCGACAAAC CTTGGGATGC ATCATTAGAG ACCTTGTTCA CGAGCAAAAG CAATGACTTC      1200
30  ATCGGTCCCC GACTGAATTT TGCTCTTGCT CGGCGCAATG TATTCGGCGG AGGAGAAAAT      1260
    CTTTCTTGGA ATATCGGTGG ATCGTATGAG TGGGAGACCG GCAATCGTCC CGAAAATAGC      1320
    AGCAATCGGC TGATCGATAT AAATTCGTAC AACATGAATA CGGCCGTGAA CCTCTCGTTT      1380
    CCCTCGATTG TATTTCCCGG TCTGCTGGAT AAATACTATT ACTACCCAC GACTACGACT      1440
    TTTCAGGCTT CTGCCACCGC GCTGAACAGG GCACACTACT TTAGCATGTA CTCTTTCGGC      1500
35  TTTTCGACCA CCTACGAATT TCAGCCCTCC AAGGAACACC GGCATGCTAT TTTCCCGCTC      1560
    AAGCTCAACT ACAACCTCCT GGGGCATCAG ACAGAACTT TCCAGGCCAT TACGGCGAAC      1620
    AATCCGCCCC TGCTGCTCAG CCTTCAGAGT CAGTTCCTTG CTCAAATGGG GTATATCTAT      1680
    ACGTTCAACA AATCCGTTTC AGAGAAAAGT CCTCATCATC TTTGGATGCA ATTCGGACTA      1740
    TCCGAGGCAG GCAATCTCCT GAATCTGATC TATCTGGCAG CCGGCAAGAA GTACAGCGAC      1800
40  ACCAAGAATT TCGTCGGCGT CCCCTTCTCT CAGTTCATCA AAGCCACGGG AGAACTGCGC      1860
    TATTCCCTATA CCATAGACCG CAATCAGTCA CTGGCAACCC GTTTCGGGAC AGGCGTGATA      1920
    TATAGCTATG GCAATATGCG AGTGGCACCC TATAGCGAGC AGTTCATATG AGGCGGTGCC      1980
    AATAGTATCA GAGCTTTCAC CGTCCGTAGC ATCGGCCCCG GACGGTTCOA TCCGGATTCC      2040
    GACAATCAGT ATTCCTATTT GGATCAGGTG GGCGAATTCA AACTCGAAGC CAACGTGGAA      2100
45  TATAGAGGCA AGCTTTTCGG GGATCTCCAC GCAGCCGTTT TCCTCGATGC GGGCAACGTT      2160
    TGGCTCTTGA GGGAGGATTC TTCCCGTCCG GGCGGTGCTC TGTCCGAAGT GGGATCGGTG      2220
    AGCAATTTCC TGAATAGCAT CGTCTCGGC ACCGGTGTGCG GCCTTCGCTA CGATCTGGCA      2280
    TTTCTCGTCC TTCGTGTCGA TGTCGGCTTC GGTCTCCACC TTCCTTACAA TACGGGTAAG      2340
    AAAGGTTACT ACAATATCCC ACGCTTTAAG GATGCCATCG GTTTCATTT GGCTGTCGGC      2400
50  TATCCCTTC      2409

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(2) INFORMATION FOR SEQ ID NO:17

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 60 (D) TOPOLOGY: circular

- (A) LENGTH: 2625 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

5

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

15

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...2625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

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20  GTCGAATCTA AATTGTTATG TCTTATGAGA AAAAGAATTC TACAACTTTT CCTGACCGCA      60
    TTGCTGCTGG CATTAGGCTC CTCTCTCGCC ATAGCGCAAA CAGTGGTGAC CGGTAAGGTG      120
    ATCGATTGAG AAACGTCCGA ACCGCTCATC GGTGTATCCG TAAGCACCGG TCAGGGAGCA      180
    TCCCTCCGCG GTGTAACCAC CGATATGGAT GGTGGCTTCC GATTTCGAAGT ACCGGCCAAA      240
25  TCTGTCTTGA CTTTCCGTTG CGTAGGTTAT GCTACCGTAA CTCGCTCTAT AGGCAGAGGT      300
    TCTCAAGAAG ACCTCGGTAC GATTCTCCTC GATCCCCAGG CCATCGGCTT GGATGAGATT      360
    CAGGTAATAG CCTCTGTGGT GCCCAAAGAC CGTATGACGC CGGTACCCGT TTCCAATATC      420
    CGTGTGGCTG ATATTCAGGC AGCATCGTTG AATGTCGAAT TTCCCGAACG GGTAAATCC      480
    ACTCCCTCTA CCTATACGAC AAAAGGAAGC GGAGGTTTCG GTGATGGTCG TACCAATGTG      540
30  CGTGGATTCG AACTTACAA CTTCGGTGTA CTCATCAACG GAGTTCCTGT CAATGGTATG      600
    GAAGACGGGA AAGTATATTG GAGCAATTGG AGTGGTCTGA TGAATCAAGC CAGTACCATT      660
    CAGATTGAGC GCGGACTCGG AGCCTCCAAG CTCGGTATCA GCTCGGTAGG TGGTACGATG      720
    AACATTATCA CGAAGACTAC GGACGCCAAC ACCGGAGGTT CGGCTTATGT CCGGTATGGGT      780
    AATGATGGAT TGCACAAAGA ATCGTTCCTC ATTTCTACGG GTATGAACGA CGGTTGGGCT      840
35  ATCACCATTG CAGGCTCCCA TATGACGGGT CTGGGTTATG TGAAGGGGCT GAAGGGACGT      900
    GCATTCTCTT ACTTCTTCAA CGTTTCGAAG AAGTTCAATG AACGTCATAC CCTCTCTCTT      960
    ACCGGATTCT GTGCACCACA ATGGCACAAAC CAACGTTCTT CCAAATATTC TGTAGCCGAC      1020
    TATGACAAAT ACGGCATCCG TCACAATCAA TCCTTCGGCT ATCTGCGAGG CGAACTGACT      1080
    CCTACGGCTT ATGCTTACAA TACGTACCAC AAGCCCCAGT TCTCGCTGAA CCACTTCTGG      1140
40  AAGATGGATG AAAAATACCTC TCTTTATACC gCANCCCTACG CATCTTTGGC TACCGGTGGA      1200
    GGTCGTCGCG CTTATGGAAA GAACAGTAAG TGGGTATTGA TCAACTACAA CACCGGACAA      1260
    CCCTATGAAC AAACAAAGGT GACTCCCGAT GGACTTATCG ACTACGATGC CGTACTGGCT      1320
    GCCAATGCTG CGGCGAGCAA TGGCTCGGAA GCAATTTTTG CCCTTGGCTC CAACTCTCAC      1380
    AAGTGGTTCT GTCTACTCTC TTCATTCAAG AAGAACTTA ATAGTTCGCT GACTTTGACA      1440
45  GCCGGATACG ATGGGCGTTA CTACCGTGGC GACCACTATG ACAAGATCAC CGATCTGCTC      1500
    GCGGGTAGCT ACTACATAGA GGATCCCAAG ACAAGCTCG CATACCATGC GGAAGGTCAG      1560
    CAACTGAAAG TGGGTGACAT TGTAATTCGG GACTACACAG GCGAAATCAT GTGGCACGGC      1620
    CTCTTCGCAC AGATGGAGCA TTCGTCCGAA TGGATCGATG CATTCGTATC AGGATCTATC      1680
    AACTACGAAC TATACCGCAA TCACAACATAT GGCGGTAGCA AGTCCACCGG CTACCTGCCC      1740
50  GGCATGATCG CGTGGAAGAG CTTCTTCCG TGGAGTGGCA AGGCAGGTCT GAGCTACAAG      1800
    TTCGCACAGG GACACAATGT ATTGCGCAAT GGCGGTTTCT TCACACGTGC ACCACTCTTT      1860
    GGCAATATCT ATGCTGCGGG GGCTATCATT CCCAATGACA AAGCCAATAT GGAAGGTG      1920
    CTTACAGGAG AGGTCGGCTA TGGATTACAG AATCACAAAA ACTTCGAGTT CAATATCAAC      1980
    GGATACTATA CGAAGTGGAT GGATCGCGTG ACCTCGAAGA GAATCGGAAA CGAGTATGTT      2040
55  TATCTCAATG GCCTTGATGC TGTTCACTGT GGGGTAGAGG CTGAGGTCAG CTATCGTCCCT      2100
    ATTCGTCAGA TCGACCTTCG CCGTATGTTT TCTCTCGGTG ACTGGACTTG GCAAAACAAT      2160
    GTAAGTTACA CTCTTACGA CGAAGCCGGC AATGAGACAG GGCAGGATAT AACCTATATC      2220
    AAGGGTCTTC ACGTCGGAGA TGCAGCACAG ATGACGGCTG CTGTATCGGC AGACATAGAG      2280
    CTGTTCAAGG GTTTCATGT CATAGGTAAG TACAACCTCC TTGGCAAAGA CTATGCAGGA      2340
60  TTCAACCCCG CAACGCGTAA TGCACAGCAG TACGAAGCGG ATGGCAAAGA AATCGTGGAA      2400

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(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- 5 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
15 (A) NAME/KEY: misc_feature
(B) LOCATION 1...1026
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

20	AGTTTTTATC	AAGAAATAGA	CAGACTTATG	AAAAAGTATT	TGTTATATGC	CTCGTTGCTA	60
	ACGAGTGTTC	TGCTCTTTTC	CTGTTCAAAG	AACAATCCTA	ACGAGCCGGT	GGAAGACAGA	120
	TCCATCGAAA	TTTCTATAAG	GGTAGATGAT	TTCACCAAAA	CGGGTGAGGC	AGTACGCTAT	180
	GAAAGGAATC	AAGGAAGTGC	TGCCGAAAGG	CTCATTACCA	ATCTTTACCT	CTTGTTGTTC	240
	GATCAGTCAG	GGGCGAATCC	GGCGAAATAC	TATATTACCG	GTAACACTTT	CACCGGAGGG	300
	ACCTGGCTTC	CTGACGATAT	GAAGGTGAAG	TTGGATATGA	CACAATCCGA	GGCCGGAGAG	360
25	CGCAAAGTAT	ATGTCGTAGC	CAATGTTGAT	AATGCGGTTA	AAACGGCTCT	TGATGCTGTC	420
	GCTAACGAAA	GCGATTTGCA	GACTGTAAAG	AGGACGACTG	CAATGCCGTG	GTGACCGAT	480
	ATAGCCTCTC	CTTTCCTGAT	GTCCGGAAAC	AAGACACACG	ACTTCTTGGC	CAATCGTCTT	540
	TTGGACAATG	TGCCCCTTGT	GCGTGCCATT	GCCAAGGTGG	AGCTGAATAT	CTCGCTGAGT	600
	GAGAAATTC	AGATTGTGCC	GATAATTGTC	AATGGTAGTT	TGAGTGAGTT	CAAGTTCAGA	660
30	TACGTAAACT	TCGACAAGGA	GACCTACGTA	GTGAAGCCAA	CGACCAAGCC	GGACAATCTC	720
	ATTAGTTCTG	CTAATGGTGT	TTGGCCTCAG	ATTACAGATT	GGACTGTATG	GGGTGCTTCC	780
	TTAAATACTT	CTCCTGCTCC	GGATGCGGGC	ACAGGTTATA	CATTGGATGC	AAATGGCAAG	840
	GTAACGGCAC	TACGGATTGT	TACCTATCTG	AATGAGCGCG	ATAGCAAAGG	GGCTACGGTA	900
	GAGGTCGCAT	TGCCTCGTGT	GGATGATGGC	ACCCTTCCTC	CTCCGGAATT	CGGTCCGGAG	960
35	CTTTATCGTT	TGCCTTTGCC	GGACAAGATC	CTGCGCAATC	ATTGGTACAA	GTATGAAGTC	1020
	GAGATT						1026

- 40 (2) INFORMATION FOR SEQ ID NO:21
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2634 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
50 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
55 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2634
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

10

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AAACAGATAG TTATGACAGT AAAGCGCGCA GTGCGAATAG CACTTCTCAC GCTGATAGGC      60
ATTCTTTTTT CCTCACCTTC TCTTGTTTCGG GCGCAAAGTC TTTTCAGCAC CGAACATGTC      120
TTGCAACTAT ACAACAAGAT ACTCTATGGA GAGTCGGCGG CGGATACCGT CGCAGAGAAA      180
ACGGCAGGTG AGTCGGCATT TCCTTTTATA GACAAACTCA TCAATCTCGG CCGCACTTTC      240
15 CTCGGCAAAC CATATCGCTA TCGCGGTCCT TCCCCATGGC CGATGGACTG CTCGGGCTAT      300
GTGTCTTACC TCTACTCCAA ATTCGACATC AAACCTCCAC GTGGTGCGGC AGCACAGAGC      360
CAATATACGA ATCCTATCGA GCGCGAGGAT GTTCGTCCGG GCGACCTCCT TTTTTTCAAA      420
GGCCGCAATG CACGCAGCAA CCGTATCGGG CATGTAGCTT TGGTCGTATC TGTCGATGAA      480
GATGATATTA CCATGATGCA CAGCCGCAAT TCGCGAGGGA TCGTGATCGA AAAACTCAAT      540
20 CGCAGTGCAT ACTTCTCCCG TCGCTTGGTG AGCTATGGCA GGGTACCCGG AGCCAAGAGA      600
GTGATCCAC  GAAAAAGT                                     618

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(2) INFORMATION FOR SEQ ID NO:23

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc feature

40

(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

```

45 Asn Arg Asn Arg Asn Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys
   1           5           10           15
Ser Leu Cys Phe Ile Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn
   20           25           30
Val Arg Asn Ser Gln Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys
   35           40           45
50 Pro Ser Asp Ser Val Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu
   50           55           60
Glu Phe Arg Asn Lys Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu
   65           70           75           80
Tyr Glu Asn Arg Leu Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp
55   85           90           95
Leu Tyr Gly Glu Asp Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly
   100          105          110
Ala Gly Thr Asp Val Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser
   115          120          125
60 Ser Phe Val Met Pro Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly

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Ser Asn Ala Arg Ala Leu Asp Leu Arg Tyr Glu Asp Glu Leu His Arg
      100      105      110
Val Ile Ile His Gly Ile Leu His Leu Cys Gly Leu Lys Asp Lys Ser
      115      120      125
5  Lys Lys Asp Glu Ala Gln Met Arg Ala Ala Glu Glu Lys Ala Leu Val
      130      135      140
Met Leu Arg Glu Thr Ile Gly Ser Glu Leu Ser Leu Leu His Thr
      145      150      155

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10 (2) INFORMATION FOR SEQ ID NO:25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

25 (A) NAME/KEY: misc feature

(B) LOCATION 1...395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

```

30  Lys Ser Lys Thr Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly
    1      5      10      15
Ala Ile Ala Leu Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr
    20      25      30
35  Gly Gln Leu Pro Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly
    35      40      45
Ser Asn Trp Phe Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu
    50      55      60
Asn Asp Asn Asn Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly
    65      70      75      80
40  Ser Leu Ser Val Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu
    85      90      95
Gln Ile Asn Gly Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu
    100      105      110
45  Gln Glu Ile Asn Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe
    115      120      125
Asp Val Val Asn Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His
    130      135      140
Leu Ile Pro Trp Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser
    145      150      155      160
50  Glu Trp Ser Lys Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val
    165      170      175
Met Met Ala Phe Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala
    180      185      190
55  Gln Ala Ala His Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys
    195      200      205
Lys Thr Pro Val Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe
    210      215      220
Gln Gly Met Ala Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly
    225      230      235      240
60  Phe Asn Ala Ile Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn

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      Asn Ala Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr
      165 170 175
Val Asn Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp
      180 185 190
5  Phe Asn Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly
      195 200 205
Thr Lys Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu
      210 215 220
10 Thr Phe Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp
      225 230 235 240
Tyr Ala Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly
      245 250 255
Gln Val Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro
      260 265 270
15 Glu Pro Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val
      275 280 285
Tyr Phe Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn
      290 295 300
20 Val Tyr Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys
      305 310 315 320
Val Val Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met
      325 330 335
Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys
      340 345 350
25 Tyr Gly Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser
      355 360 365
Glu Gln Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr
      370 375 380
30 Ala Ala Glu
      385

```

(2) INFORMATION FOR SEQ ID NO:27

```

      (i) SEQUENCE CHARACTERISTICS:
35      (A) LENGTH: 195 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein
40

      (iii) HYPOTHETICAL: YES

      (vi) ORIGINAL SOURCE:
45      (A) ORGANISM: Porphyromonas gingivalis

      (ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...195

50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

Val Ile Gly Ile Ile Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val
1      5      10      15
Phe Val Asn Asn Val Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe
55      20      25      30
Leu Gly Val Ser Lys Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala
      35      40      45
Val Thr Phe Val Leu Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln
      50      55      60
60 Lys Phe Val Leu Asp Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala

```

	Val	Leu	Ser	Pro	Glu	Leu	Phe	Leu	Lys	Thr	Asn	Ser	Thr	Asn	Leu	Ser
				180					185					190		
	Gln	Gly	Leu	Lys	Phe	Gln	Pro	Gly	Leu	Arg	Val	Glu	Asp	Asn	Cys	Gln
			195					200					205			
5	Asn	Cys	Gly	Phe	Asn	Gln	Val	Arg	Ile	Asn	Gly	Leu	Glu	Gly	Ala	Tyr
		210					215					220				
	Ser	Gln	Ile	Leu	Ile	Asp	Ser	His	Pro	Ile	Phe	Ser	Ser	Leu	Ala	Gly
		225				230					235					240
10	Val	Tyr	Gly	Leu	Glu	Gln	Met	Pro	Ala	Asn	Met	Ile	Glu	Arg	Val	Glu
					245					250					255	
	Val	Ile	Arg	Gly	Gly	Gly	Ser	Ala	Leu	Phe	Gly	Ser	Asn	Ala	Val	Gly
				260					265					270		
	Gly	Val	Ile	Asn	Val	Ile	Thr	Lys	Glu	Pro	Leu	Arg	Asn	Ser	Ala	Glu
			275					280					285			
15	Ile	Ser	His	Ser	Thr	Met	Thr	Phe	Asp	His	Ala	Lys	Gly	Trp	Gly	Ser
		290					295					300				
	Phe	Gln	Asn	Thr	Thr	Gln	Phe	Asn	Gly	Ser	Met	Leu	Thr	Glu	Asp	Arg
		305				310					315					320
20	Lys	Ala	Gly	Val	Met	Val	Phe	Gly	Gln	His	Asn	Tyr	Arg	Pro	Gly	Gln
					325					330					335	
	Asp	Ile	Asp	Gly	Asp	Asn	Phe	Thr	Glu	Leu	Pro	Asn	Leu	Arg	Asn	Arg
				340					345					350		
	Ser	Leu	Gly	Phe	Arg	Ser	Tyr	Tyr	Lys	Thr	Gly	Leu	Tyr	Ser	Lys	Ala
			355					360					365			
25	Thr	Leu	Glu	Tyr	His	Ser	Met	Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Asp	Arg
		370					375					380				
	Leu	Asp	Asn	Pro	Pro	Phe	Glu	Ala	Gln	Ile	Ala	Glu	Tyr	Leu	Gln	His
						390					395					400
30	Tyr	Ile	Asn	Gly	Gly	Ser	Phe	Lys	Phe	Asp	Gln	Gly	Phe	Ser	Gly	Gly
				405						410					415	
	Lys	Asp	Phe	Phe	Ser	Leu	Tyr	Ala	Ser	Ala	Gln	Asp	Val	Gln	Arg	Arg
				420					425					430		
	Ser	Tyr	Tyr	Gly	Gly	Gly	Asp	Tyr	Thr	Glu	Asn	Leu	Leu	Asn	Gly	Ala
			435					440					445			
35	Val	Gln	Ser	Gly	Ser	Thr	Glu	Ser	Asp	Glu	Tyr	Asn	Asp	Ala	Phe	Thr
		450					455					460				
	Ala	Leu	Thr	Ser	Tyr	Gly	Thr	Thr	Lys	Gly	Phe	Asp	Leu	Gln	Gly	Gly
		465				470					475				480	
40	Gly	Met	Tyr	Arg	His	Thr	Phe	Gly	Glu	Asn	Trp	Asp	Phe	Thr	Gly	Gly
					485					490					495	
	Leu	Glu	Tyr	Ile	Tyr	Gly	Gln	Leu	Asp	Asp	Arg	Ser	Gly	Tyr	Arg	Pro
				500					505					510		
	Ser	Lys	Ile	Asp	Gln	Asn	Thr	Ser	Thr	Phe	Ser	Gln	Tyr	Asp	Gln	Leu
			515					520					525			
45	Glu	Tyr	Lys	Thr	Glu	Lys	Leu	Ser	Ala	Leu	Ile	Gly	Ala	Arg	Ile	Asp
		530					535					540				
	Tyr	Val	Leu	Leu	Asn	Gln	Asp	Gly	Lys	Arg	Tyr	Ile	Asp	Pro	Leu	Phe
		545				550					555					560
50	Ile	Phe	Ser	Pro	Arg	Ala	Asn	Val	Arg	Tyr	Asn	Pro	Asn	Lys	Asn	Leu
					565					570					575	
	Ser	Phe	Arg	Leu	Ser	Tyr	Ser	Glu	Gly	Phe	Arg	Ala	Pro	Gln	Tyr	Phe
				580					585					590		
	Asp	Glu	Asp	Leu	His	Val	Glu	Leu	Ala	Gly	Gly	Thr	Pro	Ile	Ser	Arg
			595					600					605			
55	Val	Leu	Ser	Pro	Asn	Leu	Lys	Glu	Glu	Arg	Ser	Arg	Ser	Ile	Ser	Ala
		610					615					620				
	Ser	Phe	Asp	Tyr	Tyr	His	Arg	Ala	Asp	Glu	Trp	Gln	Phe	Asn	Ile	Met
		625				630					635					640
60	Gly	Glu	Ala	Phe	Ser	Thr	Phe	Ile	Ser	Asn	Gln	Phe	Lys	Pro	Ser	Asp
					645					650					655	

				85					90					95			
		Ile	Met	Arg	Gln	Gly	Tyr	Phe	Ser	Asn	Val	Arg	Ile	Ile	Ala	Asp	Lys
				100						105				110			
5		Tyr	Val	Gly	Asn	Lys	Val	Tyr	Leu	Lys	Ile	Ile	Val	Thr	Glu	Arg	Pro
				115					120					125			
		Arg	Ile	Ser	Lys	Val	Thr	Phe	Ser	Gly	Val	Lys	Lys	Ser	Glu	Arg	Glu
				130				135					140				
		Asp	Leu	Glu	Met	Lys	Ile	Gly	Leu	Arg	Glu	Gly	Ile	Gln	Met	Thr	Arg
				145				150				155					160
10		Asn	Asn	Glu	Asp	Lys	Val	Arg	Gln	Ile	Val	Gln	Lys	Tyr	Phe	Ser	Glu
					165						170					175	
		Lys	Gly	Tyr	Arg	Asp	Ala	Ser	Ile	Arg	Ile	Thr	Gln	Glu	Pro	Asp	Leu
					180					185					190		
15		Ser	Lys	Asp	Gly	Phe	Val	Asn	Val	Leu	Ile	Ser	Ile	Glu	Lys	Lys	Ser
				195					200					205			
		Lys	Thr	Lys	Val	Asn	Glu	Ile	Tyr	Phe	Ser	Gly	Asn	Lys	Ala	Leu	Ser
				210				215					220				
		Asn	His	Lys	Leu	Arg	Met	Ala	Met	Lys	Asn	Thr	Asn	Ala	Lys	Phe	Ser
						230						235					240
20		Leu	Arg	Lys	His	Ile	Arg	Ser	Ser	Phe	Leu	Lys	Leu	Phe	Ser	Thr	His
						245					250					255	
		Lys	Phe	Val	Glu	Glu	Ser	Tyr	Arg	Glu	Asp	Leu	Val	Arg	Leu	Ile	Glu
					260					265					270		
25		Lys	Tyr	Gln	Glu	Tyr	Gly	Tyr	Arg	Asp	Ala	Glu	Ile	Leu	Thr	Asp	Ser
				275					280					285			
		Val	Val	Lys	Ala	Pro	Asp	Gly	Lys	Arg	Val	Asp	Ile	Tyr	Leu	Asn	Ile
				290				295				300					
		Glu	Glu	Gly	Gln	Lys	Tyr	Tyr	Ile	Lys	Asp	Val	Asn	Phe	Val	Gly	Asn
				305				310				315					320
30		Ser	Gln	Tyr	Pro	Ser	Glu	Tyr	Leu	Glu	Arg	Val	Leu	Gly	Ile	Lys	Ser
					325						330					335	
		Gly	Asp	Val	Tyr	Asn	Gln	Arg	Arg	Leu	Ala	Lys	Arg	Leu	Asn	Glu	Asp
					340					345					350		
35		Glu	Asp	Ala	Val	Gly	Asn	Leu	Tyr	Tyr	Asn	Asn	Gly	Tyr	Ile	Phe	Ala
				355					360					365			
		Trp	Val	Asp	Pro	Val	Glu	Thr	Asn	Val	Val	Gly	Asp	Ser	Val	Ser	Leu
				370				375					380				
		Asp	Ile	Arg	Ile	Ala	Glu	Gly	Lys	Gln	Ala	Asn	Ile	Asn	Lys	Val	Ile
						390					395						400
40		Ile	Lys	Gly	Asn	Thr	Val	Val	Tyr	Glu	Asp	Val	Val	Arg	Arg	Glu	Leu
					405						410					415	
		Tyr	Thr	Lys	Pro	Gly	Gln	Leu	Phe	Ser	Arg	Glu	Asp	Ile	Ile	Asn	Ser
					420					425					430		
45		Ile	Arg	Leu	Ile	Asn	Gln	Leu	Gly	His	Phe	Asp	Ala	Glu	Lys	Ser	Ile
				435					440					445			
		Pro	Arg	Pro	Ile	Pro	Asn	Pro	Glu	Thr	Gly	Thr	Val	Asp	Ile	Glu	Tyr
				450				455					460				
		Asp	Leu	Val	Pro	Arg	Ser	Ser	Asp	Gln	Leu	Glu	Leu	Ser	Val	Gly	Trp
				465				470				475					480
50		Ser	Gln	Ser	Gly	Leu	Leu	Phe	Arg	Gly	Ala	Ile	Lys	Phe	Thr	Asn	Phe
					485						490					495	
		Ser	Val	Gly	Asn	Leu	Leu	His	Pro	Ser	Met	Tyr	Lys	Lys	Gly	Ile	Ile
					500				505						510		
55		Pro	Gln	Gly	Asp	Gly	Gln	Thr	Leu	Ser	Leu	Ser	Ala	Gln	Thr	Asn	Gly
				515					520					525			
		Lys	Tyr	Tyr	Gln	Gln	Tyr	Ser	Val	Thr	Phe	Met	Asp	Pro	Trp	Phe	Gly
				530				535					540				
		Gly	Lys	Arg	Pro	Asp	Met	Phe	Ser	Phe	Ser	Ala	Phe	Tyr	Ser	Lys	Thr
				545			550				555						560
60		Thr	Ala	Ile	Asp	Ser	Lys	Phe	Tyr	Asn	Ser	Asn	Ala	Gly	Asn	Tyr	Tyr

(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

```

5  Gln Ile Asn Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly
   1                               5                               15
   Phe Ala Leu Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu
                               20                               30
10 Val Asp Met Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met
   35                               40                               45
   Asn Glu Gln Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu
   50                               55                               60
   Ala Leu Glu Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp
   65                               70                               75                               80
15 Leu Val Phe Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile
   85                               90                               95
   Val Lys Lys Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly
   100                               105                               110
   Pro Glu Gly Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile
   115                               120                               125
20 Gln Asp Glu Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn
   130                               135                               140
   Tyr Gln Met Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser
   145                               150                               155                               160
25 Pro Ser Ile Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser
   165                               170                               175
   Lys

```

(2) INFORMATION FOR SEQ ID NO:31

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

```

50 Arg Ile Asn Lys Gln His Glu Met Lys Lys Phe Phe Leu Met Leu Leu
   1                               5                               10                               15
   Met Ala Leu Pro Leu Ser Leu Leu Ala Gln Lys Val Ala Val Val Asn
   20                               25                               30
   Thr Glu Glu Ile Ile Ser Lys Met Pro Glu Gln Val Ala Ala Thr Lys
   35                               40                               45
55 Gln Leu Asn Glu Leu Ala Glu Lys Tyr Arg Leu Asp Leu Lys Ser Met
   50                               55                               60
   Asp Asp Glu Phe Ala Lys Lys Thr Glu Glu Phe Val Lys Glu Lys Asp
   65                               70                               75                               80
60 Ser Leu Leu Glu Asn Ile Arg Asn Arg Arg Gln Gln Glu Leu Gln Asp

```

	Gly	Gly	Phe	Thr	Ala	Asp	Tyr	Gly	Asp	Lys	Met	Ser	Ser	Val	Leu	Asp
	225					230					235					240
	Ile	Arg	Tyr	Lys	Gln	Pro	Gln	Glu	Lys	Glu	Gly	Ala	Val	Leu	Leu	Gly
					245					250						255
5	Met	Leu	Gln	Ser	Ser	Ala	Tyr	Tyr	Gly	Ser	Ser	Ala	Gly	Ala	Phe	Ser
				260					265					270		
	Gln	Ile	Thr	Gly	Val	Arg	Tyr	Lys	Ser	Ala	Lys	Ser	Leu	Leu	Gly	Thr
			275					280					285			
10	Thr	Asp	Thr	Lys	Ala	Glu	Tyr	Asp	Pro	Ile	Tyr	Ala	Asp	Gly	Gln	Thr
	290						295					300				
	Phe	Met	Thr	Tyr	Arg	Phe	Ser	Pro	Lys	Leu	Ser	Val	Ser	Phe	Leu	Gly
	305					310					315					320
	Asn	Ile	Ser	Gln	Thr	Arg	Tyr	Lys	Phe	Val	Pro	Gln	Thr	Arg	Glu	Thr
					325					330					335	
15	Ser	Phe	Gly	Thr	Leu	Ser	Asp	Ala	Lys	Lys	Leu	Lys	Ile	Phe	Phe	Asp
				340					345					350		
	Gly	Gln	Glu	Gln	Asp	Arg	Phe	Leu	Thr	Tyr	Phe	Gly	Ala	Phe	Ser	Met
			355					360					365			
20	Asn	Phe	Val	Pro	Asp	Asp	Lys	Gln	Arg	His	Thr	Val	Thr	Leu	Ser	Ala
	370						375					380				
	Phe	Asn	Ser	Asn	Glu	Arg	Glu	Thr	Tyr	Asp	Ile	Gln	Gly	Glu	Tyr	Phe
	385				390						395					400
	Leu	Asn	Asp	Val	Gln	Leu	Gly	Ala	Asp	Gly	Thr	Ala	Ser	Met	Ala	Ser
					405					410					415	
25	Gly	Ser	Glu	Asn	Ser	Asn	Gly	Leu	Gly	Ile	Gly	Arg	Asn	His	Glu	His
				420					425					430		
	Ala	Arg	Asn	Arg	Leu	Ser	Tyr	Arg	Val	Leu	Asn	Met	Gly	Tyr	Arg	Gly
			435					440					445			
30	Glu	Met	Lys	Leu	Asn	Glu	Lys	His	Arg	Leu	Gln	Ala	Gly	Val	Ser	Ala
	450						455					460				
	Gln	Met	Glu	Lys	Ile	Ala	Asp	His	Ile	Ser	Glu	Trp	Glu	Arg	Arg	Asp
	465					470					475					480
	Ser	Val	Gly	Tyr	Asn	Leu	Pro	His	Ser	Glu	Thr	Val	Leu	Leu	Met	Tyr
					485					490					495	
35	Asn	Asn	Leu	Tyr	Ala	Asp	Thr	Gln	Met	Arg	Gly	Thr	Arg	Leu	Ser	Ala
				500					505					510		
	Phe	Val	Gln	Asp	Arg	Phe	Asn	Phe	Ser	Met	Gly	Gly	Gly	Thr	Phe	Ser
			515					520					525			
40	Leu	Ile	Pro	Gly	Ile	Arg	Ala	Ser	Trp	Trp	Ser	Phe	Asn	Lys	Glu	Leu
	530						535					540				
	Leu	Val	Ser	Pro	Arg	Ile	Ser	Val	Gly	Tyr	Ser	Pro	Glu	Ser	Asn	Pro
	545					550					555					560
	Ala	Leu	Val	Leu	Arg	Ala	Ala	Ala	Gly	Leu	Tyr	Tyr	Gln	Ala	Pro	Phe
					565					570					575	
45	Tyr	Lys	Glu	Leu	Arg	Gln	Thr	His	Lys	Asp	Ala	Glu	Gly	Asn	Asn	Val
				580					585					590		
	Val	Val	Leu	Asn	Glu	Lys	Ile	Arg	Ser	Gln	Gly	Ala	Phe	His	Ile	Leu
			595					600					605			
50	Ala	Gly	Ala	Asp	Tyr	Thr	Phe	Glu	Met	Gly	Gly	Arg	Lys	Tyr	Lys	Phe
	610						615					620				
	Thr	Ala	Glu	Ala	Tyr	Tyr	Lys	Ser	Leu	Phe	Asn	Ile	Asn	Pro	Tyr	Ile
	625					630					635					640
	Ile	Glu	Asn	Val	Lys	Ile	Arg	Tyr	Leu	Gly	Glu	Asn	Ile	Gly	Ser	Gly
					645					650					655	
55	Tyr	Ala	Ala	Gly	Ile	Asp	Leu	Lys	Leu	Phe	Gly	Glu	Leu	Val	Pro	Gly
				660					665					670		
	Val	Asp	Ser	Trp	Leu	Thr	Ala	Ser	Ile	Ile	Lys	Ala	Arg	Gln	Lys	Leu
			675					680					685			
60	Asp	Gly	Tyr	Gly	Ser	Leu	Pro	Leu	Met	Asn	Ala	Pro	Thr	Tyr	Asn	Phe
	690						695						700			


```

      180      185      190
Gln Ala Asp Val Thr Leu Thr Tyr Phe His Thr Asp His Lys Asp Leu
      195      200      205
5  Ile Leu Ser Ser Pro Asp Tyr Ala Asn Asn Ile Thr Thr Tyr Ile Asn
      210      215      220
Ala Asp Lys Ala Arg Met Ser Gly Ile Glu Ala Leu Leu Ser Tyr Asp
225      230      235      240
Phe Gly Ser Leu Phe Ala Asn Lys Phe Ser Leu Arg Ala Phe Ala Asn
      245      250      255
10 Ala Thr Ile Met Leu Asn Ser Glu Met Lys Lys Ser Gln Thr Asp Ala
      260      265      270
Pro Trp Ser Glu Met Tyr Tyr Val Arg Lys Gln Asn Ile Thr Phe Gly
      275      280      285
15 Ile Glu Tyr Arg Gly Lys Glu Gly Leu Glu Val Met Leu Asn Gly Arg
      290      295      300
Phe Met Gly Arg Arg Ile Glu Gln Asn Trp Tyr Ala Tyr Tyr Pro Glu
305      310      315      320
Val Arg Pro Glu Leu Gln Gln Leu Leu Ala Ala Glu Glu Pro Glu Leu
      325      330      335
20 Ala Ala Gln Gly Leu Leu Arg His Pro Gln Ala Met Val Phe Asn Ala
      340      345      350
Ser Ala Tyr Tyr His Met Asn Lys Tyr Leu Thr Phe Gly Val Asn Leu
      355      360      365
Asn Asn Ile Leu Asp Glu Leu Tyr Thr Glu Lys Asp Gly Tyr His Met
25      370      375      380
Pro Gly Arg Asn Ile Met Gly Lys Val Met Val Asn Phe
385      390      395

```

(2) INFORMATION FOR SEQ ID NO:34

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

35

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

40

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Porphyromonas gingivalis*

45

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...484

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

```

50 Gly Arg Ala Ser Ser Pro Tyr Arg Gln Met Asp Gly Ile Leu Asn Asp
   1      5      10      15
Glu Tyr Arg Gln Ala Ser Met Asn Arg Phe Ser Asn His Trp Pro Cys
      20      25      30
Ile Leu Val Gly Phe Val Leu Trp Phe Val Ser Ala Ser Arg Thr Val
      35      40      45
55 Ala Gln Asn Ala Ser Glu Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala
   50      55      60
Val Leu Ser Glu Ala Asp Val Leu Arg Ile Ala Leu Ser Glu Asn Ala
65      70      75      80
Thr Val Lys Val Ala Asp Met Asp Val Arg Lys Gln Glu Tyr Ala Arg
60      85      90      95

```

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

```

Phe His Asn Phe Asp Phe Leu Asn Gly Ile Lys Leu Phe Ser Met Ala
1      5      10      15
Asn Asn Thr Leu Leu Ala Lys Thr Arg Arg Tyr Val Cys Leu Val Gly
15      20      25      30
Phe Cys Trp Leu Met Ala Met Met His Leu Ser Gly Gln Glu Val Thr
35      40      45
Met Trp Gly Asp Ser His Gly Val Ala Pro Asn Gln Val Arg Arg Thr
50      55      60
20 Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln
65      70      75      80
Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys Val Thr
85      90      95
25 Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp Leu Pro
100      105      110
Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser Lys Glu
115      120      125
Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg Arg Phe
130      135      140
30 Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser Arg Ser
145      150      155      160
Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly Arg Pro
165      170      175
35 Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly
180      185      190
Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn Tyr Arg
195      200      205
Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala
210      215      220
40 Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile
225      230      235      240
Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp Pro Arg
245      250      255
45 Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala
260      265      270
Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly
275      280      285
Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile
290      295      300
50 Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile
305      310      315      320
Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg
325      330      335
55 Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser
340      345      350
Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr
355      360      365
Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp
370      375      380
60 Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser

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Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
 165 170 175
 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
 180 185 190
 5 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
 195 200 205
 Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
 210 215 220
 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
 10 225 230 235 240
 Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe
 245 250 255
 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
 260 265 270
 15 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
 275 280 285
 Ser Phe Ala Leu Lys
 290

20 (2) INFORMATION FOR SEQ ID NO:37

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

30

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

35 (A) NAME/KEY: misc_feature

(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

40 Gly Lys Leu Gln Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu
 1 5 10 15
 Leu Ala Leu Gly Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala
 20 25 30
 Val Ser Glu Lys Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly
 35 40 45
 45 Gln Asp Phe Ala Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro
 50 55 60
 Ile Asp Ser Val Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr
 65 70 75 80
 50 Thr Arg Phe Ser Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala
 85 90 95
 Arg Gln Leu Ala His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala
 100 105 110
 Met Arg Ala Ala Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro
 115 120 125
 55 Ala Asp Ala Gln Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg
 130 135 140
 Glu Asn Asn Met Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu
 145 150 155 160
 60 Tyr Ile Asp Thr Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr Thr

	His	Tyr	Asp	Ser	Ile	Ile	Pro	Leu	Pro	Ile	Ser	Thr	Phe	Pro	Asp	Ser	
			195					200					205				
	Ile	Leu	Ala	Tyr	Arg	Gln	Thr	Pro	Ser	Leu	Ile	Arg	Lys	Gly	Asp	Gln	
		210				215						220					
5	Phe	Asn	Leu	Ala	Lys	Leu	His	Glu	Glu	Arg	Gln	Thr	Ile	Ser	Ala	Leu	
	225					230					235					240	
	Leu	Arg	Asp	Asn	Gly	Tyr	Tyr	Tyr	Phe	Arg	Pro	Gln	Asp	Ile	Ile	Tyr	
					245					250					255		
10	Glu	Ala	Asp	Thr	Leu	Leu	Val	Arg	Gly	Ala	Val	Cys	Leu	Arg	Ala	Lys	
			260						265						270		
	Leu	Ser	Glu	Asp	Thr	Pro	Pro	Gln	Ala	Met	Arg	Pro	Trp	Arg	Ile	Gly	
		275						280					285				
	Lys	Arg	Thr	Ala	Val	Leu	Leu	Gly	Met	Asn	Gly	Glu	Ser	Pro	Thr	Asp	
	290						295					300					
15	Ser	Leu	Glu	Val	Glu	Asp	Met	Lys	Val	Leu	Tyr	Tyr	Arg	Lys	Met	Pro	
	305					310					315					320	
	Val	Arg	Pro	Lys	Ile	Leu	Ala	Lys	Arg	Phe	Arg	Phe	Phe	Ser	Gly	Asn	
					325					330					335		
20	Leu	Tyr	Arg	Gln	Lys	Asp	Asp	Glu	Thr	Thr	Arg	Lys	Ser	Leu	Ala	Arg	
				340					345					350			
	Leu	Gly	Ala	Phe	Ser	Val	Ile	Asp	Leu	Asn	Phe	Leu	Gln	Arg	Asp	Ser	
		355						360					365				
	Ile	Ser	Gly	Leu	Leu	Asp	Val	Arg	Leu	Leu	Thr	Thr	Leu	Asp	Lys	Pro	
	370					375						380					
25	Trp	Asp	Ala	Ser	Leu	Glu	Thr	Leu	Phe	Thr	Ser	Lys	Ser	Asn	Asp	Phe	
	385					390					395				400		
	Ile	Gly	Pro	Gly	Leu	Asn	Phe	Ala	Leu	Ala	Arg	Arg	Asn	Val	Phe	Gly	
				405					410						415		
30	Gly	Gly	Glu	Asn	Leu	Ser	Trp	Asn	Ile	Gly	Gly	Ser	Tyr	Glu	Trp	Glu	
				420					425					430			
	Thr	Gly	Asn	Arg	Pro	Glu	Asn	Ser	Ser	Asn	Arg	Leu	Ile	Asp	Ile	Asn	
			435					440					445				
	Ser	Tyr	Asn	Met	Asn	Thr	Ala	Val	Asn	Leu	Ser	Phe	Pro	Ser	Ile	Val	
	450					455						460					
35	Phe	Pro	Gly	Leu	Leu	Asp	Lys	Tyr	Tyr	Tyr	Tyr	Pro	Thr	Thr	Thr	Thr	
	465					470					475					480	
	Phe	Gln	Ala	Ser	Ala	Thr	Ala	Leu	Asn	Arg	Ala	His	Tyr	Phe	Ser	Met	
				485						490					495		
40	Tyr	Ser	Phe	Gly	Phe	Ser	Thr	Thr	Tyr	Glu	Phe	Gln	Pro	Ser	Lys	Glu	
			500						505					510			
	His	Arg	His	Ala	Ile	Phe	Pro	Leu	Lys	Leu	Asn	Tyr	Asn	Leu	Leu	Gly	
			515					520					525				
	His	Gln	Thr	Glu	Thr	Phe	Gln	Ala	Ile	Thr	Ala	Asn	Asn	Pro	Pro	Leu	
	530						535					540					
45	Leu	Leu	Ser	Leu	Gln	Ser	Gln	Phe	Leu	Ala	Gln	Met	Gly	Tyr	Ile	Tyr	
	545					550					555					560	
	Thr	Phe	Asn	Lys	Ser	Val	Ser	Glu	Lys	Ser	Pro	His	His	Leu	Trp	Met	
				565						570					575		
50	Gln	Phe	Gly	Leu	Ser	Glu	Ala	Gly	Asn	Leu	Leu	Asn	Leu	Ile	Tyr	Leu	
			580						585					590			
	Ala	Ala	Gly	Lys	Lys	Tyr	Ser	Asp	Thr	Lys	Asn	Phe	Val	Gly	Val	Pro	
			595					600					605				
	Phe	Ser	Gln	Phe	Ile	Lys	Ala	Thr	Gly	Glu	Leu	Arg	Tyr	Ser	Tyr	Thr	
	610					615						620					
55	Ile	Asp	Arg	Asn	Gln	Ser	Leu	Ala	Thr	Arg	Phe	Gly	Thr	Gly	Val	Ile	
	625					630					635					640	
	Tyr	Ser	Tyr	Gly	Asn	Met	Arg	Val	Ala	Pro	Tyr	Ser	Glu	Gln	Phe	Tyr	
				645						650					655		
60	Val	Gly	Gly	Ala	Asn	Ser	Ile	Arg	Ala	Phe	Thr	Val	Arg	Ser	Ile	Gly	
			660						665					670			

					165				170					175		
	Pro	Pro	Val	Ala	Leu	Gly	Asn	Ser	Leu	Pro	Ser	Ala	Tyr	Lys	Val	Gly
				180					185					190		
5	Ile	Ser	Glu	Gly	Ser	Pro	Leu	Ser	Pro	Ile	Val	Leu	Asp	Glu	Glu	Arg
			195					200					205			
	Lys	Ala	Ile	Ala	Arg	His	Met	Arg	Asn	Asn	Gly	Phe	Trp	Lys	Phe	Ser
		210					215					220				
	Ala	Glu	Asp	Val	Tyr	Tyr	Glu	Ala	Asp	Thr	Thr	Val	Ser	Gly	Gly	Ser
	225					230					235				240	
10	Gly	Thr	Lys	Ser	Ala	Asp	Leu	Lys	Leu	Val	Val	Asn	Gly	Ile	Gly	Arg
					245					250					255	
	Tyr	Pro	Tyr	Arg	Ile	Gly	Arg	Val	Phe	Phe	His	Ala	Asp	Tyr	Asp	Pro
				260					265					270		
	Leu	Glu	Ser	Asp	Phe	Arg	Val	Gln	Glu	Leu	Pro	Arg	Ile	Asp	Ser	Ile
			275					280					285			
15	Ser	Arg	Gly	Asp	Tyr	Thr	Val	Tyr	Tyr	Gly	Ser	Arg	Gly	Arg	Tyr	Ile
		290					295					300				
	Arg	Ala	Ser	Ala	Leu	Thr	Arg	Ser	Val	Ser	Val	Thr	Pro	Gly	Ala	Phe
	305					310					315				320	
20	Phe	Cys	Glu	Asp	Asp	Val	Glu	Arg	Ser	Tyr	Ile	Lys	Leu	Asn	Ala	Leu
				325						330					335	
	Pro	Ile	Val	Arg	Asn	Val	Asn	Ile	Arg	Phe	Val	Glu	His	Asn	Gly	Lys
				340					345					350		
	Asp	Glu	Ile	Ala	Leu	Ala	Asp	Ser	Ser	Arg	Leu	Val	Asp	Cys	Tyr	Ile
			355				360						365			
25	Leu	Thr	Val	Pro	Ala	Lys	Ser	Lys	Ser	Phe	Glu	Ala	Glu	Val	Leu	Gly
		370					375					380				
	Thr	Asn	Ser	Ala	Gly	Asp	Phe	Gly	Ala	Ala	Leu	Ser	Leu	Gly	Phe	Thr
	385					390					395				400	
30	Asp	Arg	Asn	Leu	Phe	Arg	Gly	Ala	Glu	Met	Phe	Asn	Ile	Lys	Leu	Lys
				405					410						415	
	Gly	Ala	Tyr	Glu	Ala	Ile	Arg	Lys	Gly	Ser	His	Ser	Phe	Met	Glu	Tyr
			420						425					430		
	Gly	Val	Glu	Ser	Ser	Leu	Arg	Phe	Pro	Arg	Leu	Leu	Phe	Pro	Phe	Ile
			435					440					445			
35	Ser	Asp	Glu	Thr	Arg	Arg	Arg	Leu	Arg	Ala	Ser	Thr	Glu	Trp	Lys	Ile
		450					455					460				
	Gly	Tyr	Asn	Tyr	Gln	Thr	Arg	Pro	Glu	Phe	Asp	Arg	Val	Ile	Leu	Ser
					470					475					480	
40	Ala	Gln	Leu	Asn	Tyr	Ser	Trp	Gln	Thr	Tyr	Leu	His	Asn	Arg	Leu	Arg
				485						490					495	
	His	Thr	Ile	Arg	Leu	Leu	Asp	Val	Asp	Tyr	Leu	His	Leu	Pro	Tyr	Ile
				500					505					510		
	Asp	Pro	Asp	Phe	Ala	Gln	Ser	Leu	Pro	Pro	Thr	Thr	Ala	Leu	Tyr	Asn
			515					520					525			
45	Tyr	Thr	Glu	Gln	Phe	Ile	Leu	Gly	Ser	Ala	Tyr	Ile	Leu	Asn	Tyr	Thr
		530					535					540				
	Thr	Ala	Ser	Ser	Met	Glu	Arg	Thr	Val	Ser	Asn	Pro	Phe	Thr	Ala	Arg
					550						555				560	
50	Phe	Ser	Ile	Gln	Thr	Ala	Gly	Asn	Leu	Leu	Gln	Ala	Ile	Ser	Tyr	Leu
				565						570					575	
	Thr	Asp	Ser	Pro	Lys	Asp	Glu	His	Gly	Leu	Tyr	Lys	Met	Phe	Gly	Leu
			580						585					590		
	His	Tyr	Ala	Gln	Phe	Val	Lys	Leu	Asp	Leu	Asp	Leu	Ala	Lys	Thr	Val
			595					600					605			
55	Leu	Leu	Glu	Lys	Asp	Asn	Thr	Leu	Ala	Leu	His	Leu	Gly	Phe	Gly	Leu
		610					615					620				
	Ala	Phe	Pro	Tyr	Gly	Asn	Ala	Arg	His	Ile	Pro	Phe	Glu	Leu	Arg	Tyr
					630						635				640	
60	Phe	Ala	Gly	Gly	Ser	Asn	Ser	Val	Arg	Gly	Trp	Ser	Val	Arg	Thr	Leu

	Arg	Thr	Asn	Val	Arg	Gly	Phe	Asp	Thr	Tyr	Asn	Phe	Gly	Val	Leu	Ile
				180					185					190		
	Asn	Gly	Val	Pro	Val	Asn	Gly	Met	Glu	Asp	Gly	Lys	Val	Tyr	Trp	Ser
			195					200					205			
5	Asn	Trp	Ser	Gly	Leu	Met	Asn	Gln	Ala	Ser	Thr	Ile	Gln	Ile	Gln	Arg
		210					215					220				
	Gly	Leu	Gly	Ala	Ser	Lys	Leu	Gly	Ile	Ser	Ser	Val	Gly	Gly	Thr	Met
		225				230					235					240
10	Asn	Ile	Ile	Thr	Lys	Thr	Thr	Asp	Ala	Asn	Thr	Gly	Gly	Ser	Ala	Tyr
					245						250				255	
	Val	Gly	Met	Gly	Asn	Asp	Gly	Leu	His	Lys	Glu	Ser	Phe	Ser	Ile	Ser
				260					265					270		
	Thr	Gly	Met	Asn	Asp	Gly	Trp	Ala	Ile	Thr	Ile	Ala	Gly	Ser	His	Met
			275					280					285			
15	Thr	Gly	Leu	Gly	Tyr	Val	Lys	Gly	Leu	Lys	Gly	Arg	Ala	Phe	Ser	Tyr
		290					295					300				
	Phe	Phe	Asn	Val	Ser	Lys	Lys	Phe	Asn	Glu	Arg	His	Thr	Leu	Ser	Leu
		305				310					315					320
20	Thr	Gly	Phe	Gly	Ala	Pro	Gln	Trp	His	Asn	Gln	Arg	Ser	Ser	Lys	Tyr
					325					330					335	
	Ser	Val	Ala	Asp	Tyr	Asp	Lys	Tyr	Gly	Ile	Arg	His	Asn	Gln	Ser	Phe
				340					345					350		
	Gly	Tyr	Leu	Arg	Gly	Glu	Leu	Thr	Pro	Thr	Ala	Tyr	Ala	Tyr	Asn	Thr
			355					360					365			
25	Tyr	His	Lys	Pro	Gln	Phe	Ser	Leu	Asn	His	Phe	Trp	Lys	Met	Asp	Glu
		370					375					380				
	Asn	Thr	Ser	Leu	Tyr	Thr	Ala	Unk	Tyr	Ala	Ser	Leu	Ala	Thr	Gly	Gly
		385				390					395					400
30	Gly	Arg	Arg	Ala	Tyr	Gly	Lys	Asn	Ser	Lys	Trp	Val	Leu	Ile	Asn	Tyr
				405						410					415	
	Asn	Thr	Gly	Gln	Pro	Tyr	Glu	Gln	Thr	Lys	Val	Thr	Pro	Asp	Gly	Leu
				420					425					430		
	Ile	Asp	Tyr	Asp	Ala	Val	Leu	Ala	Ala	Asn	Ala	Ala	Ala	Ser	Asn	Gly
			435					440					445			
35	Ser	Glu	Ala	Ile	Phe	Ala	Leu	Gly	Ser	Asn	Ser	His	Lys	Trp	Phe	Gly
		450					455					460				
	Leu	Leu	Ser	Ser	Phe	Lys	Lys	Lys	Leu	Asn	Ser	Ser	Leu	Thr	Leu	Thr
		465				470					475					480
40	Ala	Gly	Tyr	Asp	Gly	Arg	Tyr	Tyr	Arg	Gly	Asp	His	Tyr	Asp	Lys	Ile
					485					490					495	
	Thr	Asp	Leu	Leu	Gly	Gly	Ser	Tyr	Tyr	Ile	Glu	Asp	Pro	Lys	Thr	Lys
				500					505					510		
	Leu	Ala	Tyr	His	Ala	Glu	Gly	Gln	Gln	Leu	Lys	Val	Gly	Asp	Ile	Val
			515					520					525			
45	Asn	Arg	Asp	Tyr	Thr	Gly	Glu	Ile	Met	Trp	His	Gly	Leu	Phe	Ala	Gln
		530					535					540				
	Met	Glu	His	Ser	Ser	Glu	Trp	Ile	Asp	Ala	Phe	Val	Ser	Gly	Ser	Ile
		545				550					555					560
50	Asn	Tyr	Glu	Leu	Tyr	Arg	Asn	His	Asn	Tyr	Gly	Gly	Ser	Lys	Ser	Thr
					565					570					575	
	Gly	Tyr	Leu	Pro	Gly	Val	Ser	Pro	Trp	Lys	Ser	Phe	Leu	Pro	Trp	Ser
				580					585					590		
	Gly	Lys	Ala	Gly	Leu	Ser	Tyr	Lys	Phe	Ala	Gln	Gly	His	Asn	Val	Phe
			595					600					605			
55	Ala	Asn	Gly	Gly	Phe	Phe	Thr	Arg	Ala	Pro	Leu	Phe	Gly	Asn	Ile	Tyr
		610					615					620				
	Ala	Ala	Gly	Ala	Ile	Ile	Pro	Asn	Asp	Lys	Ala	Asn	Met	Glu	Lys	Val
		625				630					635					640
60	Leu	Thr	Gly	Glu	Val	Gly	Tyr	Gly	Phe	Thr	Asn	His	Lys	Asn	Phe	Glu
					645					650					655	

				85					90				95			
	Leu	Asn	Lys	Gln	Val	Ala	Gln	Arg	Lys	Gln	Met	Val	Gln	Leu	Leu	Asp
				100					105					110		
5	Asn	Glu	Val	Lys	Glu	Leu	Gln	Ser	Asp	Ile	Asp	Ser	Met	Thr	Gly	Val
			115					120					125			
	Cys	His	Gln	Leu	Ser	Val	Glu	Glu	Lys	Ala	Arg	Ser	Asp	Glu	Tyr	Ala
		130					135					140				
	Gln	Ala	Leu	Gln	Ser	Met	Gln	Lys	Arg	Lys	Arg	Ser	Leu	Asp	Arg	Ile
	145					150					155				160	
10	Leu	Phe	Ile	Ser	Ser	Ala	Lys	Ser	Phe	Asp	Glu	Gly	Met	Arg	Arg	Met
				165					170						175	
	Arg	Phe	Leu	Glu	Gln	Tyr	Ala	Ser	Ala	Tyr	Lys	Leu	Ala	Ser	Val	Arg
			180					185					190			
	Leu	Arg	Asp	Thr	Arg	Ser	Lys	Leu	Glu	Thr	Glu	Arg	Ala	Thr	Val	Glu
15			195				200						205			
	Asp	Ala	Lys	Lys	Glu	Lys	Gly	His	Leu	Leu	Val	Ile	Arg	Glu	Glu	Glu
		210					215					220				
	Lys	Lys	Lys	Leu	Glu	Gly	Gln	Gln	Ala	Glu	Gln	Arg	Arg	Gln	Val	Gln
	225					230					235				240	
20	Ala	Leu	Gly	Ala	Lys	Gln	Lys	Asp	Leu	Glu	Ala	Gln	Leu	Arg	Lys	Gln
				245					250						255	
	Lys	Lys	Gln	Ala	Glu	Ala	Leu	Asn	Arg	Lys	Ile	Glu	Lys	Gln	Ile	Ala
			260					265						270		
	Lys	Glu	Ile	Glu	Ala	Ala	Glu	Arg	Arg	Ala	Arg	Glu	Glu	Arg	Glu	Arg
25			275					280					285			
	Leu	Ala	Arg	Glu	Ala	Lys	Ala	Lys	Gly	Lys	Pro	Val	Pro	Ala	Glu	Pro
		290				295						300				
	Glu	Arg	Lys	Ala	Glu	Thr	Lys	Gly	Gly	Tyr	Ala	Met	Asp	Ala	Ser	Glu
	305					310					315				320	
30	Arg	Ala	Leu	Ser	Gly	Ser	Phe	Ala	Gln	Asn	Lys	Gly	Arg	Leu	Pro	Gly
				325					330						335	
	Pro	Val	Arg	Gly	Arg	Tyr	Arg	Ile	Val	Ser	Asp	Phe	Gly	Val	His	Gln
			340					345						350		
	His	Ser	Glu	Leu	Lys	Lys	Val	Gln	Val	Asn	Asn	Gly	Gly	Ile	Asp	Ile
35			355				360						365			
	Ala	Val	Ala	Thr	Gly	Ser	Asp	Ala	Thr	Ser	Val	Phe	Asp	Gly	Val	Val
		370				375					380					
	Ser	Ser	Val	Phe	Val	Ile	Pro	Gly	Tyr	Asn	Ser	Ala	Val	Met	Val	Arg
	385				390					395					400	
40	His	Gly	Asn	Tyr	Ile	Thr	Val	Tyr	Ala	Asn	Leu	Ser	Lys	Val	Tyr	Val
				405						410					415	
	Asn	Ser	Gly	Thr	Arg	Val	Lys	Thr	Gly	Gln	Ala	Leu	Gly	Arg	Ala	Tyr
			420					425					430			
	Thr	Asp	Pro	Ser	Asn	Asn	Gln	Thr	Ile	Ile	His	Phe	Glu	Ile	Trp	Lys
45			435				440						445			
	Glu	Arg	Ser	Lys	Gln	Asn	Pro	Arg	Leu	Trp	Leu	Arg				
		450				455					460					

(2) INFORMATION FOR SEQ ID NO:42

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

60

- (vi) ORIGINAL SOURCE:

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

10 (A) NAME/KEY: misc feature

(B) LOCATION 1...878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

15	Ala	Asp	Ser	Ile	Arg	Tyr	Pro	Leu	Tyr	Phe	Phe	Gly	Arg	Asn	Arg	Lys	1	5	10	15
	Lys	Cys	Phe	Arg	Glu	Pro	Ile	Pro	Thr	Leu	Tyr	Asn	Lys	Asn	Met	Ile	20	25	30	
	Gly	Lys	Lys	Ile	Phe	Phe	Ile	Leu	Leu	Ala	Leu	Ile	Ala	Phe	Ser	Gly	35	40	45	
20	Leu	Asn	Ala	Ala	Thr	Asp	Thr	Glu	Phe	Lys	Tyr	Pro	Thr	Asp	Ala	Asn	50	55	60	
	Ile	Ile	Gly	His	Val	Lys	Asp	Ser	Lys	Thr	Gly	Glu	His	Leu	Val	Gly	65	70	75	80
	Ile	Thr	Ile	Ala	Ile	Lys	Gly	Thr	Thr	Phe	Gly	Thr	Ser	Thr	Asp	Ala	85	90	95	
25	Thr	Gly	His	Tyr	Tyr	Leu	Arg	Asn	Leu	Arg	Pro	Gly	Glu	Ile	Thr	Leu	100	105	110	
	Ile	Met	Arg	Gly	Met	Gly	Tyr	Lys	Ser	Gln	Glu	Arg	Val	Val	Arg	Val	115	120	125	
30	Glu	Lys	Asp	Lys	Thr	Ile	Glu	Val	Asn	Phe	Glu	Ala	Glu	Glu	Asp	Ala	130	135	140	
	Ile	Asn	Leu	Asp	Glu	Val	Val	Ile	Ser	Ala	Asn	Arg	Glu	Leu	Thr	Leu	145	150	155	160
	Arg	Arg	Leu	Ala	Pro	Thr	Leu	Val	Asn	Val	Leu	Asn	Glu	Lys	Val	Phe	165	170	175	
35	Ser	Gln	Val	Asn	Ala	Ser	Asn	Leu	Ala	Gln	Gly	Leu	Ser	Phe	Gln	Pro	180	185	190	
	Gly	Val	Arg	Val	Glu	Asn	Asn	Cys	Gln	Asn	Cys	Gly	Phe	Asn	Gln	Val	195	200	205	
40	Arg	Ile	Asn	Gly	Leu	Asp	Gly	Arg	Tyr	Ala	Gln	Ile	Leu	Ile	Asp	Ser	210	215	220	
	Arg	Pro	Ile	Met	Ser	Ala	Leu	Ala	Gly	Val	Tyr	Gly	Leu	Glu	Gln	Ile	225	230	235	240
	Pro	Ala	Asn	Met	Ile	Glu	Arg	Val	Glu	Val	Val	Arg	Gly	Gly	Gly	Ser	245	250	255	
45	Ala	Leu	Tyr	Gly	Ser	Ser	Ala	Ile	Ala	Gly	Val	Val	Asn	Ile	Ile	Thr	260	265	270	
	Lys	Glu	Pro	Ser	His	Asn	Ser	Phe	Thr	Phe	Asn	Glu	Ser	Leu	Ser	Phe	275	280	285	
50	Thr	Gly	Phe	Ser	Lys	Leu	Asp	Asn	Asn	Thr	Asn	Phe	Asn	Ala	Ser	Ile	290	295	300	
	Val	Ser	Asp	Asp	Asn	Arg	Ala	Gly	Ala	Met	Val	Phe	Gly	Gln	Ala	Arg	305	310	315	320
	Tyr	Arg	Asn	His	Trp	Asp	Ala	Asn	Asn	Asp	Gly	Tyr	Ser	Glu	Leu	Gly	325	330	335	
55	Lys	Ile	Asp	Ala	Arg	Ser	Leu	Gly	Ala	His	Ser	Tyr	Leu	Arg	Leu	Ser	340	345	350	
	Asp	Tyr	Ser	Lys	Leu	Thr	Gly	Glu	Phe	His	Thr	Ile	Ser	Glu	Phe	Arg	355	360	365	
60	Arg	Gly	Gly	Asp	Arg	Ile	Asp	Leu	Pro	Pro	His	Val	Val	Gly	Val	Ala				

850 855 860
 Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe
 865 870 875

5 (2) INFORMATION FOR SEQ ID NO:44

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

20 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

25 Lys Gln Ile Val Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu
 1 5 10 15
 Thr Leu Ile Gly Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln
 20 25 30
 30 Ser Leu Phe Ser Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu
 35 40 45
 Tyr Gly Glu Ser Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu
 50 55 60
 Ser Ala Phe Pro Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe
 65 70 75 80
 35 Leu Gly Lys Pro Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp
 85 90 95
 Cys Ser Gly Tyr Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu
 100 105 110
 Pro Arg Gly Ala Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg
 40 115 120 125
 Glu Asp Val Arg Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala
 130 135 140
 Arg Ser Asn Arg Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu
 145 150 155 160
 45 Asp Asp Ile Thr Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile
 165 170 175
 Glu Lys Leu Asn Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr
 180 185 190
 Gly Arg Val Pro Gly Ala Lys Arg Val Ile Pro Arg Lys Ser
 50 195 200 205

(2) INFORMATION FOR SEQ ID NO:45

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 337 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...151

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

```

Met Ala Lys Ile Asn Phe Tyr Ala Glu Gly Val Ser Leu Pro Arg Ile
1      5      10      15
Arg Arg Arg Ile Val Gly Lys Trp Ile Ala Glu Val Cys Ser Arg Tyr
20     20     25     30
Gly Lys Ala Val Gly Glu Ile Ser Tyr Leu Phe Cys Asp Asp Glu Tyr
35     40     45
Ile Leu Lys Ala Asn Gln Glu Phe Leu Asp His Asp Tyr Tyr Thr Asp
50     55     60
25 Ile Ile Thr Phe Asp Ser Cys Glu Ala Asp Thr Val Asn Gly Asp Leu
65     70     75     80
Leu Ile Ser Leu Asp Thr Val Arg Ser Asn Ala Arg Ala Leu Asp Leu
85     90     95
30 Arg Tyr Glu Asp Glu Leu His Arg Val Ile Ile His Gly Ile Leu His
100    105    110
Leu Cys Gly Leu Lys Asp Lys Ser Lys Lys Asp Glu Ala Gln Met Arg
115    120    125
Ala Ala Glu Glu Lys Ala Leu Val Met Leu Arg Glu Thr Ile Gly Ser
130    135    140
35 Glu Leu Ser Leu Leu His Thr
145    150

```

(2) INFORMATION FOR SEQ ID NO:47

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

50 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...391

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

```

Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly Ala Ile Ala Leu
1      5      10      15
60 Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr Gly Gln Leu Pro

```

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

5 (B) LOCATION 1...385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

```

10 Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala Leu Ala
    1      5      10      15
    Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr Thr Gln
        20      25      30
    Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala Ser Asp
        35      40      45
15 His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu Ser Gly
    50      55      60
    Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val Pro Thr
    65      70      75      80
    Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg Leu Gln
    85      90      95
20 Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys Glu Arg
    100      105      110
    Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe Asp Leu
    115      120      125
25 Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His Ile Ile
    130      135      140
    Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu Asn Ala
    145      150      155      160
    Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr Val Asn
    165      170      175
30 Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp Phe Asn
    180      185      190
    Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly Thr Lys
    195      200      205
35 Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu Thr Phe
    210      215      220
    Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp Tyr Ala
    225      230      235      240
    Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly Gln Val
    245      250      255
40 Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro Glu Pro
    260      265      270
    Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val Tyr Phe
    275      280      285
45 Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn Val Tyr
    290      295      300
    Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys Val Val
    305      310      315      320
    Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met Lys Leu
    325      330      335
50 Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys Tyr Gly
    340      345      350
    Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser Glu Gln
    355      360      365
55 Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr Ala Ala
    370      375      380
    Glu
    385

```

60 (2) INFORMATION FOR SEQ ID NO:49

(B) LOCATION 1...833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

5	Met	Lys	Gln	Leu	Asn	Ile	Ile	Ser	Phe	Ile	Ile	Ala	Phe	Leu	Phe	Leu
	1				5					10				15		
	Gly	Thr	Ser	Ala	Ser	Ala	Gln	Gln	Ser	Gly	Gly	Ser	Val	Thr	Gly	Thr
				20					25				30			
	Val	Val	Asp	Lys	Ser	Ser	Lys	Glu	Pro	Ile	Ala	Tyr	Val	Gln	Val	Phe
10			35					40					45			
	Val	Lys	Gly	Thr	Thr	Leu	Gly	Thr	Ser	Thr	Asp	Ala	Asn	Gly	Asn	Tyr
		50					55					60				
	Ser	Ile	Lys	Gly	Ile	Pro	Ser	Gly	Asn	Gln	Thr	Ile	Val	Ala	Arg	Leu
	65				70					75					80	
15	Met	Gly	Tyr	Ser	Thr	Cys	Glu	Glu	Lys	Val	His	Ile	Glu	Lys	Gly	Gly
					85					90					95	
	Ser	Arg	His	Val	Asp	Leu	Tyr	Leu	Thr	Glu	Glu	Ile	Leu	Ser	Leu	Asp
				100					105					110		
	Gly	Val	Val	Val	Ser	Ala	Asn	Arg	Asn	Glu	Thr	Phe	Arg	Arg	Gln	Ala
20				115				120					125			
	Pro	Ser	Leu	Val	Thr	Val	Leu	Ser	Pro	Glu	Leu	Phe	Leu	Lys	Thr	Asn
		130					135					140				
	Ser	Thr	Asn	Leu	Ser	Gln	Gly	Leu	Lys	Phe	Gln	Pro	Gly	Leu	Arg	Val
	145					150					155				160	
25	Glu	Asp	Asn	Cys	Gln	Asn	Cys	Gly	Phe	Asn	Gln	Val	Arg	Ile	Asn	Gly
					165					170					175	
	Leu	Glu	Gly	Ala	Tyr	Ser	Gln	Ile	Leu	Ile	Asp	Ser	His	Pro	Ile	Phe
				180					185					190		
	Ser	Ser	Leu	Ala	Gly	Val	Tyr	Gly	Leu	Glu	Gln	Met	Pro	Ala	Asn	Met
30			195					200					205			
	Ile	Glu	Arg	Val	Glu	Val	Ile	Arg	Gly	Gly	Gly	Ser	Ala	Leu	Phe	Gly
		210					215					220				
	Ser	Asn	Ala	Val	Gly	Gly	Val	Ile	Asn	Val	Ile	Thr	Lys	Glu	Pro	Leu
	225				230					235					240	
35	Arg	Asn	Ser	Ala	Glu	Ile	Ser	His	Ser	Thr	Met	Thr	Phe	Asp	His	Ala
					245					250					255	
	Lys	Gly	Trp	Gly	Ser	Phe	Gln	Asn	Thr	Thr	Gln	Phe	Asn	Gly	Ser	Met
				260					265					270		
	Leu	Thr	Glu	Asp	Arg	Lys	Ala	Gly	Val	Met	Val	Phe	Gly	Gln	His	Asn
40			275					280					285			
	Tyr	Arg	Pro	Gly	Gln	Asp	Ile	Asp	Gly	Asp	Asn	Phe	Thr	Glu	Leu	Pro
		290					295					300				
	Asn	Leu	Arg	Asn	Arg	Ser	Leu	Gly	Phe	Arg	Ser	Tyr	Tyr	Lys	Thr	Gly
	305				310					315					320	
45	Leu	Tyr	Ser	Lys	Ala	Thr	Leu	Glu	Tyr	His	Ser	Met	Gln	Glu	Tyr	Arg
					325					330					335	
	Arg	Gly	Gly	Asp	Arg	Leu	Asp	Asn	Pro	Phe	Glu	Ala	Gln	Ile	Ala	
				340					345				350			
	Glu	Tyr	Leu	Gln	His	Tyr	Ile	Asn	Gly	Gly	Ser	Phe	Lys	Phe	Asp	Gln
50			355					360					365			
	Gly	Phe	Ser	Gly	Gly	Lys	Asp	Phe	Phe	Ser	Leu	Tyr	Ala	Ser	Ala	Gln
		370					375					380				
	Asp	Val	Gln	Arg	Arg	Ser	Tyr	Tyr	Gly	Gly	Gly	Asp	Tyr	Thr	Glu	Asn
	385				390					395					400	
55	Leu	Leu	Asn	Gly	Ala	Val	Gln	Ser	Gly	Ser	Thr	Glu	Ser	Asp	Glu	Tyr
					405					410					415	
	Asn	Asp	Ala	Phe	Thr	Ala	Leu	Thr	Ser	Tyr	Gly	Thr	Thr	Lys	Gly	Phe
				420					425					430		
	Asp	Leu	Gln	Gly	Gly	Gly	Met	Tyr	Arg	His	Thr	Phe	Gly	Glu	Asn	Trp
60			435					440					445			

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

5

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...891

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

	Met	Tyr	Lys	Lys	Ile	Ile	Ala	Val	Ala	Ala	Leu	Phe	Cys	Ala	Ser	Ile	
	1				5					10					15		
15	Gly	Ile	Leu	Lys	Gly	Gln	Ser	Ser	Asp	Leu	Thr	Pro	Gln	Asp	Thr	Ile	
			20						25					30			
	Tyr	Ser	Pro	Glu	Ile	Ser	Tyr	Ala	Lys	Pro	Ile	His	Lys	Thr	Ile	Ala	
			35					40					45				
	Ser	Ile	Glu	Ile	Glu	Gly	Met	Arg	Ser	Phe	Asp	Asp	Phe	Val	Leu	Arg	
		50					55				60						
20	Asn	Leu	Ser	Gly	Leu	Ala	Val	Gly	Asp	Glu	Val	Leu	Ile	Pro	Gly	Asp	
	65				70					75					80		
	Ala	Met	Ser	Ala	Ala	Val	Asn	Arg	Ile	Met	Arg	Gln	Gly	Tyr	Phe	Ser	
				85				90						95			
	Asn	Val	Arg	Ile	Ile	Ala	Asp	Lys	Tyr	Val	Gly	Asn	Lys	Val	Tyr	Leu	
25				100				105						110			
	Lys	Ile	Ile	Val	Thr	Glu	Arg	Pro	Arg	Ile	Ser	Lys	Val	Thr	Phe	Ser	
			115					120					125				
	Gly	Val	Lys	Lys	Ser	Glu	Arg	Glu	Asp	Leu	Glu	Met	Lys	Ile	Gly	Leu	
		130					135					140					
30	Arg	Glu	Gly	Ile	Gln	Met	Thr	Arg	Asn	Asn	Glu	Asp	Lys	Val	Arg	Gln	
	145					150					155					160	
	Ile	Val	Gln	Lys	Tyr	Phe	Ser	Glu	Lys	Gly	Tyr	Arg	Asp	Ala	Ser	Ile	
				165						170					175		
	Arg	Ile	Thr	Gln	Glu	Pro	Asp	Leu	Ser	Lys	Asp	Gly	Phe	Val	Asn	Val	
35				180				185						190			
	Leu	Ile	Ser	Ile	Glu	Lys	Lys	Ser	Lys	Thr	Lys	Val	Asn	Glu	Ile	Tyr	
			195					200					205				
	Phe	Ser	Gly	Asn	Lys	Ala	Leu	Ser	Asn	His	Lys	Leu	Arg	Met	Ala	Met	
		210					215					220					
40	Lys	Asn	Thr	Asn	Ala	Lys	Phe	Ser	Leu	Arg	Lys	His	Ile	Arg	Ser	Ser	
	225					230					235					240	
	Phe	Leu	Lys	Leu	Phe	Ser	Thr	His	Lys	Phe	Val	Glu	Glu	Ser	Tyr	Arg	
				245						250					255		
	Glu	Asp	Leu	Val	Arg	Leu	Ile	Glu	Lys	Tyr	Gln	Glu	Tyr	Gly	Tyr	Arg	
45				260				265						270			
	Asp	Ala	Glu	Ile	Leu	Thr	Asp	Ser	Val	Val	Lys	Ala	Pro	Asp	Gly	Lys	
			275					280					285				
	Arg	Val	Asp	Ile	Tyr	Leu	Asn	Ile	Glu	Glu	Gly	Gln	Lys	Tyr	Tyr	Ile	
		290					295					300					
50	Lys	Asp	Val	Asn	Phe	Val	Gly	Asn	Ser	Gln	Tyr	Pro	Ser	Glu	Tyr	Leu	
	305					310					315					320	
	Glu	Arg	Val	Leu	Gly	Ile	Lys	Ser	Gly	Asp	Val	Tyr	Asn	Gln	Arg	Arg	
				325						330					335		
	Leu	Ala	Lys	Arg	Leu	Asn	Glu	Asp	Glu	Asp	Ala	Val	Gly	Asn	Leu	Tyr	
55				340					345					350			
	Tyr	Asn	Asn	Gly	Tyr	Ile	Phe	Ala	Trp	Val	Asp	Pro	Val	Glu	Thr	Asn	
			355					360					365				
	Val	Val	Gly	Asp	Ser	Val	Ser	Leu	Asp	Ile	Arg	Ile	Ala	Glu	Gly	Lys	
			370				375					380					
60	Gln	Ala	Asn	Ile	Asn	Lys	Val	Ile	Ile	Lys	Gly	Asn	Thr	Val	Val	Tyr	

865 870 875 880
 Ser Asn Val His Phe Val Leu Gly Gln Glu Phe
 885 890

5 (2) INFORMATION FOR SEQ ID NO:52

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 170 amino acids

 (B) TYPE: amino acid

10 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein

 (iii) HYPOTHETICAL: YES

15

 (vi) ORIGINAL SOURCE:

 (A) ORGANISM: Porphyromonas gingivalis

 (ix) FEATURE:

20 (A) NAME/KEY: misc feature

 (B) LOCATION 1...170

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

25 Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu Ala Val Ala Phe
 1 5 10 15
 Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met Glu Tyr Ile Leu
 20 25 30
 Arg Asn Ile Pro Asp Tyr Glu Met Asn Glu Gln Leu Glu Gln Val
 35 40 45
 Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu Asn Glu Ala Gln
 50 55 60
 Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe Leu Ser Ala Ala
 65 70 75 80
 Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys Glu Gln Gln Ala
 85 90 95
 Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly Glu Leu Tyr Lys
 100 105 110
 Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu Ile Trp Asn Ala
 115 120 125
 Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met Val Leu Asp Arg
 130 135 140
 Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile Asp Ile Ser Asp
 145 150 155 160
 Leu Val Leu Ser Lys Met Gly Phe Ser Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:53

50 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 163 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

 (iii) HYPOTHETICAL: YES

 (vi) ORIGINAL SOURCE:

60 (A) ORGANISM: Porphyromonas gingivalis

	Ala	Thr	Thr	Asp	Ser	Ile	Thr	Ile	Glu	Phe	Ser	Ser	Met	Gly	Tyr	Gln
					85					90					95	
	Gly	Val	Ser	Arg	Ser	Phe	Pro	Ser	Leu	Thr	Lys	Asp	Thr	Arg	Leu	Asn
				100					105					110		
5	Val	Arg	Leu	Ala	Glu	Ala	Glu	Met	Glu	Leu	Ser	Ser	Val	Thr	Val	Gln
			115					120					125			
	Ala	Thr	Lys	Arg	Arg	Leu	Asn	Thr	Met	Glu	Arg	Val	Asn	Thr	Arg	Asp
		130					135					140				
10	Leu	Arg	Val	Asn	Ala	Gly	Pro	Thr	Gly	Gly	Val	Glu	Ser	Leu	Ile	Ser
	145					150					155					160
	Thr	Tyr	Ala	Gly	Val	Thr	Gln	Asn	Asn	Glu	Leu	Ser	Ser	Gln	Tyr	Ser
				165						170					175	
	Val	Arg	Gly	Gly	Ser	Tyr	Asp	Glu	Asn	Met	Val	Tyr	Val	Asn	Gly	Val
				180					185					190		
15	Glu	Val	Tyr	Arg	Pro	Leu	Leu	Val	Arg	Ser	Ala	Gln	Gln	Glu	Gly	Leu
			195					200					205			
	Ser	Phe	Val	Asn	Pro	Asp	Leu	Thr	Gln	Ser	Val	Gln	Phe	Ser	Ala	Gly
		210				215						220				
20	Gly	Phe	Thr	Ala	Asp	Tyr	Gly	Asp	Lys	Met	Ser	Ser	Val	Leu	Asp	Ile
	225					230					235					240
	Arg	Tyr	Lys	Gln	Pro	Gln	Glu	Lys	Glu	Gly	Ala	Val	Leu	Leu	Gly	Met
				245						250					255	
	Leu	Gln	Ser	Ser	Ala	Tyr	Tyr	Gly	Ser	Ser	Ala	Gly	Ala	Phe	Ser	Gln
				260					265					270		
25	Ile	Thr	Gly	Val	Arg	Tyr	Lys	Ser	Ala	Lys	Ser	Leu	Leu	Gly	Thr	Thr
			275					280					285			
	Asp	Thr	Lys	Ala	Glu	Tyr	Asp	Pro	Ile	Tyr	Ala	Asp	Gly	Gln	Thr	Phe
		290					295					300				
30	Met	Thr	Tyr	Arg	Phe	Ser	Pro	Lys	Leu	Ser	Val	Ser	Phe	Leu	Gly	Asn
	305					310					315					320
	Ile	Ser	Gln	Thr	Arg	Tyr	Lys	Phe	Val	Pro	Gln	Thr	Arg	Glu	Thr	Ser
				325						330					335	
	Phe	Gly	Thr	Leu	Ser	Asp	Ala	Lys	Lys	Leu	Lys	Ile	Phe	Phe	Asp	Gly
				340					345					350		
35	Gln	Glu	Gln	Asp	Arg	Phe	Leu	Thr	Tyr	Phe	Gly	Ala	Phe	Ser	Met	Asn
			355					360					365			
	Phe	Val	Pro	Asp	Asp	Lys	Gln	Arg	His	Thr	Val	Thr	Leu	Ser	Ala	Phe
		370				375						380				
40	Asn	Ser	Asn	Glu	Arg	Glu	Thr	Tyr	Asp	Ile	Gln	Gly	Glu	Tyr	Phe	Leu
	385					390					395					400
	Asn	Asp	Val	Gln	Leu	Gly	Ala	Asp	Gly	Thr	Ala	Ser	Met	Ala	Ser	Gly
				405						410					415	
	Ser	Glu	Asn	Ser	Asn	Gly	Leu	Gly	Ile	Gly	Arg	Asn	His	Glu	His	Ala
				420					425					430		
45	Arg	Asn	Arg	Leu	Ser	Tyr	Arg	Val	Leu	Asn	Met	Gly	Tyr	Arg	Gly	Glu
			435					440					445			
	Met	Lys	Leu	Asn	Glu	Lys	His	Arg	Leu	Gln	Ala	Gly	Val	Ser	Ala	Gln
		450					455					460				
50	Met	Glu	Lys	Ile	Ala	Asp	His	Ile	Ser	Glu	Trp	Glu	Arg	Arg	Asp	Ser
	465					470					475					480
	Val	Gly	Tyr	Asn	Leu	Pro	His	Ser	Glu	Thr	Val	Leu	Leu	Met	Tyr	Asn
				485						490					495	
	Asn	Leu	Tyr	Ala	Asp	Thr	Gln	Met	Arg	Gly	Thr	Arg	Leu	Ser	Ala	Phe
				500					505					510		
55	Val	Gln	Asp	Arg	Phe	Asn	Phe	Ser	Met	Gly	Gly	Gly	Thr	Phe	Ser	Leu
			515						520				525			
	Ile	Pro	Gly	Ile	Arg	Ala	Ser	Trp	Trp	Ser	Phe	Asn	Lys	Glu	Leu	Leu
		530					535					540				
60	Val	Ser	Pro	Arg	Ile	Ser	Val	Gly	Tyr	Ser	Pro	Glu	Ser	Asn	Pro	Ala
	545					550					555					560

[illegible]

(2) INFORMATION FOR SEQ ID NO:56

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 462 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe Asp Phe Met Thr Ala Lys
 435 440 445
 Ala Glu Leu Asp Lys Met Asn Gly Met Gly Ile Pro Glu Gln
 450 455 460

5

(2) INFORMATION FOR SEQ ID NO:57

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 526 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

20 (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

25

	Met	Ala	Asn	Asn	Thr	Leu	Leu	Ala	Lys	Thr	Arg	Arg	Tyr	Val	Cys	Leu	
	1				5					10					15		
	Val	Gly	Phe	Cys	Trp	Leu	Met	Ala	Met	Met	His	Leu	Ser	Gly	Gln	Glu	
				20					25					30			
30	Val	Thr	Met	Trp	Gly	Asp	Ser	His	Gly	Val	Ala	Pro	Asn	Gln	Val	Arg	
			35					40					45				
	Arg	Thr	Leu	Val	Lys	Val	Ala	Leu	Ser	Glu	Ser	Leu	Pro	Pro	Gly	Ala	
		50					55					60					
	Lys	Gln	Ile	Arg	Ile	Gly	Phe	Ser	Leu	Pro	Lys	Glu	Thr	Glu	Glu	Lys	
35	65				70					75					80		
	Val	Thr	Ala	Leu	Tyr	Leu	Leu	Val	Ser	Asp	Ser	Leu	Ala	Val	Arg	Asp	
					85				90						95		
	Leu	Pro	Asp	Tyr	Lys	Gly	Arg	Val	Ser	Tyr	Asp	Ser	Phe	Pro	Ile	Ser	
				100					105					110			
40	Lys	Glu	Asp	Arg	Thr	Thr	Ala	Leu	Ser	Ala	Asp	Ser	Val	Ala	Gly	Arg	
			115					120					125				
	Arg	Phe	Phe	Tyr	Leu	Ala	Ala	Asp	Ile	Gly	Pro	Val	Ala	Ser	Phe	Ser	
		130				135						140					
	Arg	Ser	Asp	Thr	Leu	Thr	Ala	Arg	Val	Glu	Glu	Val	Ala	Val	Asp	Gly	
45	145				150					155					160		
	Arg	Pro	Leu	Pro	Leu	Lys	Glu	Leu	Ser	Pro	Ala	Ser	Arg	Arg	Leu	Tyr	
				165					170					175			
	Arg	Gly	Tyr	Glu	Ala	Leu	Phe	Val	Pro	Gly	Asp	Gly	Gly	Ser	Arg	Asn	
				180					185					190			
50	Tyr	Arg	Ile	Pro	Ala	Ile	Leu	Lys	Thr	Ala	Asn	Gly	Thr	Leu	Ile	Ala	
			195					200					205				
	Met	Ala	Asp	Arg	Arg	Lys	Tyr	Asn	Gln	Thr	Asp	Leu	Pro	Glu	Asp	Ile	
			210				215					220					
	Asp	Ile	Val	Met	Arg	Arg	Ser	Thr	Asp	Gly	Gly	Lys	Ser	Trp	Ser	Asp	
55	225				230					235					240		
	Pro	Arg	Ile	Ile	Val	Gln	Gly	Glu	Gly	Arg	Asn	His	Gly	Phe	Gly	Asp	
				245					250					255			
	Val	Ala	Leu	Val	Gln	Thr	Gln	Ala	Gly	Lys	Leu	Leu	Met	Ile	Phe	Val	
				260				265						270			
60	Gly	Gly	Val	Gly	Leu	Trp	Gln	Ser	Thr	Pro	Asp	Arg	Pro	Gln	Arg	Thr	

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Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala
65      70      75      80
Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser
      85      90      95
5  Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln
      100      105      110
Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
      115      120      125
10 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
      130      135      140
Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
145      150      155      160
Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
      165      170      175
15 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
      180      185      190
Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe
      195      200      205
20 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
      210      215      220
Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
225      230      235      240
Ser Phe Ala Leu Lys
      245

```

25

(2) INFORMATION FOR SEQ ID NO:59

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 276 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear
30
(ii) MOLECULE TYPE: protein
35
(iii) HYPOTHETICAL: YES
    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Porphyromonas gingivalis
40
(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION 1...276

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

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45

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Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu Leu Ala Leu Gly
1      5      10      15
Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala Val Ser Glu Lys
      20      25      30
50 Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly Gln Asp Phe Ala
      35      40      45
Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro Ile Asp Ser Val
      50      55      60
Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr Thr Arg Phe Ser
55 65      70      75      80
Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala Arg Gln Leu Ala
      85      90      95
His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala Met Arg Ala Ala
      100      105      110
60 Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro Ala Asp Ala Gln

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	Leu	Lys	Lys	Asp	Ser	Leu	Lys	Ala	Lys	Ile	Ser	Tyr	Thr	Val	Asp	Met
	145					150					155					160
	Ala	Ser	Pro	Tyr	His	Tyr	Asp	Ser	Ile	Ile	Pro	Leu	Pro	Ile	Ser	Thr
					165					170						175
5	Phe	Pro	Asp	Ser	Ile	Leu	Ala	Tyr	Arg	Gln	Thr	Pro	Ser	Leu	Ile	Arg
				180					185					190		
	Lys	Gly	Asp	Gln	Phe	Asn	Leu	Ala	Lys	Leu	His	Glu	Glu	Arg	Gln	Thr
			195					200				205				
10	Ile	Ser	Ala	Leu	Leu	Arg	Asp	Asn	Gly	Tyr	Tyr	Tyr	Phe	Arg	Pro	Gln
		210					215					220				
	Asp	Ile	Ile	Tyr	Glu	Ala	Asp	Thr	Leu	Leu	Val	Arg	Gly	Ala	Val	Cys
	225					230					235					240
	Leu	Arg	Ala	Lys	Leu	Ser	Glu	Asp	Thr	Pro	Pro	Gln	Ala	Met	Arg	Pro
				245						250					255	
15	Trp	Arg	Ile	Gly	Lys	Arg	Thr	Ala	Val	Leu	Leu	Gly	Met	Asn	Gly	Glu
				260					265					270		
	Ser	Pro	Thr	Asp	Ser	Leu	Glu	Val	Glu	Asp	Met	Lys	Val	Leu	Tyr	Tyr
			275					280					285			
20	Arg	Lys	Met	Pro	Val	Arg	Pro	Lys	Ile	Leu	Ala	Lys	Arg	Phe	Arg	Phe
		290					295					300				
	Phe	Ser	Gly	Asn	Leu	Tyr	Arg	Gln	Lys	Asp	Asp	Glu	Thr	Thr	Arg	Lys
	305					310				315						320
	Ser	Leu	Ala	Arg	Leu	Gly	Ala	Phe	Ser	Val	Ile	Asp	Leu	Asn	Phe	Leu
				325						330					335	
25	Gln	Arg	Asp	Ser	Ile	Ser	Gly	Leu	Leu	Asp	Val	Arg	Leu	Leu	Thr	Thr
				340					345					350		
	Leu	Asp	Lys	Pro	Trp	Asp	Ala	Ser	Leu	Glu	Thr	Leu	Phe	Thr	Ser	Lys
			355					360					365			
30	Ser	Asn	Asp	Phe	Ile	Gly	Pro	Gly	Leu	Asn	Phe	Ala	Leu	Ala	Arg	Arg
		370					375					380				
	Asn	Val	Phe	Gly	Gly	Gly	Glu	Asn	Leu	Ser	Trp	Asn	Ile	Gly	Gly	Ser
	385					390					395					400
	Tyr	Glu	Trp	Glu	Thr	Gly	Asn	Arg	Pro	Glu	Asn	Ser	Ser	Asn	Arg	Leu
				405						410					415	
35	Ile	Asp	Ile	Asn	Ser	Tyr	Asn	Met	Asn	Thr	Ala	Val	Asn	Leu	Ser	Phe
				420					425					430		
	Pro	Ser	Ile	Val	Phe	Pro	Gly	Leu	Leu	Asp	Lys	Tyr	Tyr	Tyr	Tyr	Pro
			435					440					445			
40	Thr	Thr	Thr	Thr	Phe	Gln	Ala	Ser	Ala	Thr	Ala	Leu	Asn	Arg	Ala	His
		450					455					460				
	Tyr	Phe	Ser	Met	Tyr	Ser	Phe	Gly	Phe	Ser	Thr	Thr	Tyr	Glu	Phe	Gln
	465					470					475					480
	Pro	Ser	Lys	Glu	His	Arg	His	Ala	Ile	Phe	Pro	Leu	Lys	Leu	Asn	Tyr
				485						490					495	
45	Asn	Leu	Leu	Gly	His	Gln	Thr	Glu	Thr	Phe	Gln	Ala	Ile	Thr	Ala	Asn
				500					505					510		
	Asn	Pro	Pro	Leu	Leu	Leu	Ser	Leu	Gln	Ser	Gln	Phe	Leu	Ala	Gln	Met
			515					520					525			
50	Gly	Tyr	Ile	Tyr	Thr	Phe	Asn	Lys	Ser	Val	Ser	Glu	Lys	Ser	Pro	His
		530					535					540				
	His	Leu	Trp	Met	Gln	Phe	Gly	Leu	Ser	Glu	Ala	Gly	Asn	Leu	Leu	Asn
	545					550					555					560
	Leu	Ile	Tyr	Leu	Ala	Ala	Gly	Lys	Lys	Tyr	Ser	Asp	Thr	Lys	Asn	Phe
				565						570					575	
55	Val	Gly	Val	Pro	Phe	Ser	Gln	Phe	Ile	Lys	Ala	Thr	Gly	Glu	Leu	Arg
				580					585					590		
	Tyr	Ser	Tyr	Thr	Ile	Asp	Arg	Asn	Gln	Ser	Leu	Ala	Thr	Arg	Phe	Gly
			595					600					605			
60	Thr	Gly	Val	Ile	Tyr	Ser	Tyr	Gly	Asn	Met	Arg	Val	Ala	Pro	Tyr	Ser
	610						615					620				

	145		150		155		160
	Asp	Val	Lys	Asn	Pro	Leu	Leu
				165			170
5	Pro	Ser	Ala	Tyr	Lys	Val	Gly
				180			185
	Ile	Val	Leu	Asp	Glu	Glu	Arg
				195			200
	Asn	Gly	Phe	Trp	Lys	Phe	Ser
				210			215
10	Thr	Thr	Val	Ser	Gly	Gly	Ser
							230
	Val	Val	Asn	Gly	Ile	Gly	Arg
							245
15	Phe	His	Ala	Asp	Tyr	Asp	Pro
				260			265
	Leu	Pro	Arg	Ile	Asp	Ser	Ile
				275			280
	Gly	Ser	Arg	Gly	Arg	Tyr	Ile
				290			295
20	Ser	Val	Thr	Pro	Gly	Ala	Phe
							310
	Tyr	Ile	Lys	Leu	Asn	Ala	Leu
							325
25	Phe	Val	Glu	His	Asn	Gly	Lys
				340			345
	Arg	Leu	Val	Asp	Cys	Tyr	Ile
				355			360
	Phe	Glu	Ala	Glu	Val	Leu	Gly
				370			375
30	Ala	Leu	Ser	Leu	Gly	Phe	Thr
							390
	Met	Phe	Asn	Ile	Lys	Leu	Lys
							405
35	Ser	His	Ser	Phe	Met	Glu	Tyr
				420			425
	Arg	Leu	Leu	Phe	Pro	Phe	Ile
				435			440
	Ala	Ser	Thr	Glu	Trp	Lys	Ile
							455
40	Phe	Asp	Arg	Val	Ile	Leu	Ser
							470
	Tyr	Leu	His	Asn	Arg	Leu	Arg
							485
45	Tyr	Leu	His	Leu	Pro	Tyr	Ile
				500			505
	Pro	Thr	Thr	Ala	Leu	Tyr	Asn
				515			520
	Ala	Tyr	Ile	Leu	Asn	Tyr	Thr
				530			535
50	Ser	Asn	Pro	Phe	Thr	Ala	Arg
							550
	Leu	Gln	Ala	Ile	Ser	Tyr	Leu
							565
55	Leu	Tyr	Lys	Met	Phe	Gly	Leu
				580			585
	Leu	Asp	Leu	Ala	Lys	Thr	Val
				595			600
	Leu	His	Leu	Gly	Phe	Gly	Leu
							615
60	Ile	Pro	Phe	Glu	Leu	Arg	Tyr
							620

	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Gly	Arg	Thr	Asn	Val	Arg	Gly	Phe	Asp
					165					170					175	
	Thr	Tyr	Asn	Phe	Gly	Val	Leu	Ile	Asn	Gly	Val	Pro	Val	Asn	Gly	Met
				180					185					190		
5	Glu	Asp	Gly	Lys	Val	Tyr	Trp	Ser	Asn	Trp	Ser	Gly	Leu	Met	Asn	Gln
			195					200					205			
	Ala	Ser	Thr	Ile	Gln	Ile	Gln	Arg	Gly	Leu	Gly	Ala	Ser	Lys	Leu	Gly
		210					215					220				
10	Ile	Ser	Ser	Val	Gly	Gly	Thr	Met	Asn	Ile	Ile	Thr	Lys	Thr	Thr	Asp
		225				230					235					240
	Ala	Asn	Thr	Gly	Gly	Ser	Ala	Tyr	Val	Gly	Met	Gly	Asn	Asp	Gly	Leu
				245						250					255	
	His	Lys	Glu	Ser	Phe	Ser	Ile	Ser	Thr	Gly	Met	Asn	Asp	Gly	Trp	Ala
				260					265					270		
15	Ile	Thr	Ile	Ala	Gly	Ser	His	Met	Thr	Gly	Leu	Gly	Tyr	Val	Lys	Gly
			275					280					285			
	Leu	Lys	Gly	Arg	Ala	Phe	Ser	Tyr	Phe	Phe	Asn	Val	Ser	Lys	Lys	Phe
		290					295					300				
20	Asn	Glu	Arg	His	Thr	Leu	Ser	Leu	Thr	Gly	Phe	Gly	Ala	Pro	Gln	Trp
		305				310					315					320
	His	Asn	Gln	Arg	Ser	Ser	Lys	Tyr	Ser	Val	Ala	Asp	Tyr	Asp	Lys	Tyr
				325						330					335	
	Gly	Ile	Arg	His	Asn	Gln	Ser	Phe	Gly	Tyr	Leu	Arg	Gly	Glu	Leu	Thr
				340					345					350		
25	Pro	Thr	Ala	Tyr	Ala	Tyr	Asn	Thr	Tyr	His	Lys	Pro	Gln	Phe	Ser	Leu
			355					360					365			
	Asn	His	Phe	Trp	Lys	Met	Asp	Glu	Asn	Thr	Ser	Leu	Tyr	Thr	Ala	Unk
		370				375						380				
30	Tyr	Ala	Ser	Leu	Ala	Thr	Gly	Gly	Gly	Arg	Arg	Ala	Tyr	Gly	Lys	Asn
					390						395					400
	Ser	Lys	Trp	Val	Leu	Ile	Asn	Tyr	Asn	Thr	Gly	Gln	Pro	Tyr	Glu	Gln
				405						410					415	
	Thr	Lys	Val	Thr	Pro	Asp	Gly	Leu	Ile	Asp	Tyr	Asp	Ala	Val	Leu	Ala
				420					425					430		
35	Ala	Asn	Ala	Ala	Ala	Ser	Asn	Gly	Ser	Glu	Ala	Ile	Phe	Ala	Leu	Gly
			435					440					445			
	Ser	Asn	Ser	His	Lys	Trp	Phe	Gly	Leu	Leu	Ser	Ser	Phe	Lys	Lys	Lys
		450					455					460				
40	Leu	Asn	Ser	Ser	Leu	Thr	Leu	Thr	Ala	Gly	Tyr	Asp	Gly	Arg	Tyr	Tyr
		465				470					475					480
	Arg	Gly	Asp	His	Tyr	Asp	Lys	Ile	Thr	Asp	Leu	Leu	Gly	Gly	Ser	Tyr
				485						490					495	
	Tyr	Ile	Glu	Asp	Pro	Lys	Thr	Lys	Leu	Ala	Tyr	His	Ala	Glu	Gly	Gln
			500						505					510		
45	Gln	Leu	Lys	Val	Gly	Asp	Ile	Val	Asn	Arg	Asp	Tyr	Thr	Gly	Glu	Ile
			515					520					525			
	Met	Trp	His	Gly	Leu	Phe	Ala	Gln	Met	Glu	His	Ser	Ser	Glu	Trp	Ile
		530					535					540				
50	Asp	Ala	Phe	Val	Ser	Gly	Ser	Ile	Asn	Tyr	Glu	Leu	Tyr	Arg	Asn	His
		545				550					555					560
	Asn	Tyr	Gly	Gly	Ser	Lys	Ser	Thr	Gly	Tyr	Leu	Pro	Gly	Val	Ser	Pro
				565						570					575	
	Trp	Lys	Ser	Phe	Leu	Pro	Trp	Ser	Gly	Lys	Ala	Gly	Leu	Ser	Tyr	Lys
				580					585					590		
55	Phe	Ala	Gln	Gly	His	Asn	Val	Phe	Ala	Asn	Gly	Gly	Phe	Phe	Thr	Arg
			595					600					605			
	Ala	Pro	Leu	Phe	Gly	Asn	Ile	Tyr	Ala	Ala	Gly	Ala	Ile	Ile	Pro	Asn
			610				615					620				
60	Asp	Lys	Ala	Asn	Met	Glu	Lys	Val	Leu	Thr	Gly	Glu	Val	Gly	Tyr	Gly
		625				630					635					640

	65				70				75				80
	Leu	Leu	Asp	Asn	Glu	Val	Lys	Glu	Leu	Gln	Ser	Asp	Ile
					85				90				Ser
5	Thr	Gly	Val	Cys	His	Gln	Leu	Ser	Val	Glu	Glu	Lys	Ala
				100					105				Arg
	Glu	Tyr	Ala	Gln	Ala	Leu	Gln	Ser	Met	Gln	Lys	Arg	Lys
			115					120				125	Arg
	Asp	Arg	Ile	Leu	Phe	Ile	Ser	Ser	Ala	Lys	Ser	Phe	Asp
		130					135				140		Glu
10	Arg	Arg	Met	Arg	Phe	Leu	Glu	Gln	Tyr	Ala	Ser	Ala	Tyr
						150					155		Lys
	Ser	Val	Arg	Leu	Arg	Asp	Thr	Arg	Ser	Lys	Leu	Glu	Thr
				165					170				Glu
	Thr	Val	Glu	Asp	Ala	Lys	Lys	Glu	Lys	Gly	His	Leu	Leu
15				180					185				Val
	Glu	Glu	Glu	Lys	Lys	Lys	Leu	Glu	Gly	Gln	Gln	Ala	Glu
			195					200				205	Gln
	Gln	Val	Gln	Ala	Leu	Gly	Ala	Lys	Gln	Lys	Asp	Leu	Glu
		210				215					220		Ala
20	Arg	Lys	Gln	Lys	Lys	Gln	Ala	Glu	Ala	Leu	Asn	Arg	Lys
						230					235		Ile
	Gln	Ile	Ala	Lys	Glu	Ile	Glu	Ala	Ala	Glu	Arg	Arg	Ala
				245					250				Arg
	Arg	Glu	Arg	Leu	Ala	Arg	Glu	Ala	Lys	Ala	Lys	Gly	Lys
25				260					265				Pro
	Ala	Glu	Pro	Glu	Arg	Lys	Ala	Glu	Thr	Lys	Gly	Gly	Tyr
			275					280				285	Ala
	Ala	Ser	Glu	Arg	Ala	Leu	Ser	Gly	Ser	Phe	Ala	Gln	Asn
		290					295				300		Lys
30	Leu	Pro	Gly	Pro	Val	Arg	Gly	Arg	Tyr	Arg	Ile	Val	Ser
						310					315		Asp
	Val	His	Gln	His	Ser	Glu	Leu	Lys	Lys	Val	Gln	Val	Asn
				325						330			Asn
	Ile	Asp	Ile	Ala	Val	Ala	Thr	Gly	Ser	Asp	Ala	Thr	Ser
35				340					345				Val
	Gly	Val	Val	Ser	Ser	Val	Phe	Val	Ile	Pro	Gly	Tyr	Asn
			355					360				365	Ser
	Met	Val	Arg	His	Gly	Asn	Tyr	Ile	Thr	Val	Tyr	Ala	Asn
		370					375				380		Leu
40	Val	Tyr	Val	Asn	Ser	Gly	Thr	Arg	Val	Lys	Thr	Gly	Gln
						390					395		Ala
	Arg	Ala	Tyr	Thr	Asp	Pro	Ser	Asn	Asn	Gln	Thr	Ile	Ile
				405						410			His
	Ile	Trp	Lys	Glu	Arg	Ser	Lys	Gln	Asn	Pro	Arg	Leu	Trp
45				420					425				Leu
												430	Arg

(2) INFORMATION FOR SEQ ID NO:64

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 333 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: Porphyromonas gingivalis

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

5 (A) NAME/KEY: misc_feature

(B) LOCATION 1...848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

10	Met	Ile	Gly	Lys	Lys	Ile	Phe	Phe	Ile	Leu	Leu	Ala	Leu	Ile	Ala	Phe
	1				5					10					15	
	Ser	Gly	Leu	Asn	Ala	Ala	Thr	Asp	Thr	Glu	Phe	Lys	Tyr	Pro	Thr	Asp
				20					25					30		
	Ala	Asn	Ile	Ile	Gly	His	Val	Lys	Asp	Ser	Lys	Thr	Gly	Glu	His	Leu
15			35					40					45			
	Val	Gly	Ile	Thr	Ile	Ala	Ile	Lys	Gly	Thr	Thr	Phe	Gly	Thr	Ser	Thr
	50						55					60				
	Asp	Ala	Thr	Gly	His	Tyr	Tyr	Leu	Arg	Asn	Leu	Arg	Pro	Gly	Glu	Ile
	65					70					75					80
20	Thr	Leu	Ile	Met	Arg	Gly	Met	Gly	Tyr	Lys	Ser	Gln	Glu	Arg	Val	Val
				85						90					95	
	Arg	Val	Glu	Lys	Asp	Lys	Thr	Ile	Glu	Val	Asn	Phe	Glu	Ala	Glu	Glu
				100					105					110		
	Asp	Ala	Ile	Asn	Leu	Asp	Glu	Val	Val	Ile	Ser	Ala	Asn	Arg	Glu	Leu
25			115					120					125			
	Thr	Leu	Arg	Arg	Leu	Ala	Pro	Thr	Leu	Val	Asn	Val	Leu	Asn	Glu	Lys
			130					135					140			
	Val	Phe	Ser	Gln	Val	Asn	Ala	Ser	Asn	Leu	Ala	Gln	Gly	Leu	Ser	Phe
	145					150					155					160
30	Gln	Pro	Gly	Val	Arg	Val	Glu	Asn	Asn	Cys	Gln	Asn	Cys	Gly	Phe	Asn
				165						170					175	
	Gln	Val	Arg	Ile	Asn	Gly	Leu	Asp	Gly	Arg	Tyr	Ala	Gln	Ile	Leu	Ile
				180					185					190		
	Asp	Ser	Arg	Pro	Ile	Met	Ser	Ala	Leu	Ala	Gly	Val	Tyr	Gly	Leu	Glu
35			195					200					205			
	Gln	Ile	Pro	Ala	Asn	Met	Ile	Glu	Arg	Val	Glu	Val	Val	Arg	Gly	Gly
			210				215					220				
	Gly	Ser	Ala	Leu	Tyr	Gly	Ser	Ser	Ala	Ile	Ala	Gly	Val	Val	Asn	Ile
	225					230					235					240
40	Ile	Thr	Lys	Glu	Pro	Ser	His	Asn	Ser	Phe	Thr	Phe	Asn	Glu	Ser	Leu
				245						250					255	
	Ser	Phe	Thr	Gly	Phe	Ser	Lys	Leu	Asp	Asn	Asn	Thr	Asn	Phe	Asn	Ala
				260					265					270		
	Ser	Ile	Val	Ser	Asp	Asp	Asn	Arg	Ala	Gly	Ala	Met	Val	Phe	Gly	Gln
45			275					280					285			
	Ala	Arg	Tyr	Arg	Asn	His	Trp	Asp	Ala	Asn	Asn	Asp	Gly	Tyr	Ser	Glu
			290				295					300				
	Leu	Gly	Lys	Ile	Asp	Ala	Arg	Ser	Leu	Gly	Ala	His	Ser	Tyr	Leu	Arg
	305					310					315					320
50	Leu	Ser	Asp	Tyr	Ser	Lys	Leu	Thr	Gly	Glu	Phe	His	Thr	Ile	Ser	Glu
				325						330					335	
	Phe	Arg	Arg	Gly	Gly	Asp	Arg	Ile	Asp	Leu	Pro	Pro	His	Val	Val	Gly
				340					345					350		
	Val	Ala	Glu	Gln	Thr	Asp	His	Ser	Val	Phe	Ser	Gly	Asn	Leu	Lys	Tyr
55			355					360					365			
	Asp	Leu	Phe	Ser	Ser	Asn	Tyr	Lys	His	His	Phe	Gln	Ala	Tyr	Thr	Ser
			370				375					380				
	Gly	Gln	Ile	Val	Asn	Arg	Lys	Ser	Tyr	Tyr	Gly	Gly	Ile	Gly	Glu	Ile
	385					390					395					400
60	Asp	Val	Asn	Gly	His	Pro	Gly	Gly	Thr	Glu	Gly	Tyr	Pro	Ile	Pro	Gln

(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...202

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

	Met	Thr	Val	Lys	Arg	Ala	Val	Arg	Ile	Ala	Leu	Leu	Thr	Leu	Ile	Gly	
	1				5					10					15		
20	Ile	Leu	Phe	Ser	Ser	Pro	Ser	Leu	Val	Arg	Ala	Gln	Ser	Leu	Phe	Ser	
				20					25					30			
	Thr	Glu	His	Val	Leu	Gln	Leu	Tyr	Asn	Lys	Ile	Leu	Tyr	Gly	Glu	Ser	
			35					40					45				
	Ala	Ala	Asp	Thr	Val	Ala	Glu	Lys	Thr	Ala	Gly	Glu	Ser	Ala	Phe	Pro	
		50					55					60					
25	Phe	Ile	Asp	Lys	Leu	Ile	Asn	Leu	Gly	Arg	Thr	Phe	Leu	Gly	Lys	Pro	
	65					70					75					80	
	Tyr	Arg	Tyr	Arg	Gly	Pro	Ser	Pro	Trp	Pro	Met	Asp	Cys	Ser	Gly	Tyr	
					85					90					95		
	Val	Ser	Tyr	Leu	Tyr	Ser	Lys	Phe	Asp	Ile	Lys	Leu	Pro	Arg	Gly	Ala	
30				100					105					110			
	Ala	Ala	Gln	Ser	Gln	Tyr	Thr	Asn	Pro	Ile	Glu	Arg	Glu	Asp	Val	Arg	
			115					120					125				
	Pro	Gly	Asp	Leu	Leu	Phe	Phe	Lys	Gly	Arg	Asn	Ala	Arg	Ser	Asn	Arg	
		130					135					140					
35	Ile	Gly	His	Val	Ala	Leu	Val	Val	Ser	Val	Asp	Glu	Asp	Asp	Ile	Thr	
	145					150					155					160	
	Met	Met	His	Ser	Arg	Asn	Ser	Arg	Gly	Ile	Val	Ile	Glu	Lys	Leu	Asn	
					165					170					175		
	Arg	Ser	Ala	Tyr	Phe	Ser	Arg	Arg	Leu	Val	Ser	Tyr	Gly	Arg	Val	Pro	
40				180					185					190			
	Gly	Ala	Lys	Arg	Val	Ile	Pro	Arg	Lys	Ser							
			195					200									

45